GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: April 23, 2003, 12:06:52 ; Search time 172.986 Seconds
(without alignments)
3059.318 Million cell updates/sec

Title: US-09-198-779B-1
Perfect score: 235
Sequence: 1 gttttccgtctagcctcggt.....ctgcgaggtggtcaagcccc 235

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : N_Geneseq_101002:*
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21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	121	51.5	2061	21	AAA48574	cDNA encoding corn
2	75.6	32.2	1674	21	AAC47744	Zea mays DNA fragm
3	65.8	28.0	1380	20	AAX07185	Wheat S-adenosylme
4	61.6	26.2	1182	19	AAT99143	S-adenosylmethioni
5	61	26.0	1182	19	AAT99141	S-adenosylmethioni
6	59.4	25.3	1182	19	AAT99142	S-adenosylmethioni
7	54.6	23.2	399	20	AAX81128	S-adenosyl methion
8	53	22.6	1485	20	AAX07184	Soybean S-adenosyl
9	53	22.6	1518	21	AAA51037	Soybean S-adenosyl
10	51	21.7	1582	20	AAX07183	Corn S-adenosylmet
11	50.4	21.4	635	21	AAC44219	Arabidopsis thalia
12	50.4	21.4	1508	21	AAC33986	Arabidopsis thalia
13	50.4	21.4	1521	21	AAC45478	Arabidopsis thalia
14	50.4	21.4	1529	21	AAC33535	Arabidopsis thalia
15	49.8	21.2	1653	21	AAC45944	Arabidopsis thalia
16	49.8	21.2	1654	21	AAC35348	Arabidopsis thalia
17	46.6	19.8	1636	22	AAD02296	Nicotiana tabacum
18	42.4	18.0	1393	21	AAC46421	Arabidopsis thalia
19	42.4	18.0	1395	21	AAC33674	Arabidopsis thalia
20	40.2	17.1	1208	15	AAQ64204	snaC gene encoding
21	40.2	17.1	5392	15	AAQ64201	Sequence comprisin
22	40	17.0	4848	24	AAD22684	Streptomyces fradi
23	40	17.0	4848	24	AAD22686	Streptomyces fradi
c 24	39.4	16.8	1693	21	AAA75637	Nucleotide sequenc
c 25	39.4	16.8	1693	21	AAZ56005	Contig 004 from co
26	37.4	15.9	297	24	ABL72111	Corn tassel-derive
27	34.6	14.7	56485	21	AAA81476	N. meningitidis pa
c 28	34.6	14.7	349980	21	AAF21612	Neisseria meningit
c 29	34.6	14.7	837096	21	AAA81489	N. meningitidis pa
30	34.4	14.6	4403765	22	AAI99683	Mycobacterium tube
31	34.4	14.6	4411529	22	AAI99682	Mycobacterium tube
c 32	33	14.0	17512	23	ABL09034	Drosophila melanog
c 33	31.2	13.3	1844	22	AAH99804	Human protein enco
c 34	30.8	13.1	66788	23	AAS59515	Propionibacterium
c 35	30.6	13.0	606	23	AAS51580	Pseudomonas aerugi
36	30.6	13.0	657	21	AAF12426	Aspergillus oryzae
37	30.6	13.0	2247	23	ABL29661	Drosophila melanog
38	30.2	12.9	566	21	AAF08527	Fusarium venenatum
39	29.8	12.7	1519	20	AAV64373	GABA-gated chlorid
40	29.6	12.6	3550	23	ABL09035	Drosophila melanog
c 41	29.4	12.5	1683	18	AAT86246	cDNA encoding mugw
42	29.2	12.4	1557	21	AAZ49567	Maize MLO9 protein
43	29.2	12.4	2604	21	AAA48576	cDNA encoding whea
c 44	29	12.3	1086	23	ABL04431	Drosophila melanog
45	29	12.3	1221	22	AAH66738	C glutamicum codin
46	29	12.3	1239	16	AAT04566	S-adenosylmethioni
47	29	12.3	1344	22	AAF71873	Corynebacterium gl
48	29	12.3	1344	23	AAS96132	C. glutamicum gene
49	29	12.3	3205	23	ABL04430	Drosophila melanog
c 50	29	12.3	349980	22	AAH68529	C glutamicum codin

ALIGNMENTS

RESULT 1
AAA48574
ID AAA48574 standard; cDNA; 2061 BP.
XX
AC AAA48574;
XX
DT 19-SEP-2000 (first entry)
XX
DE cDNA encoding corn protein phosphatase 2A regulatory subunit A.
XX
KW Corn; protein phosphatase 2A; protein phosphorylation modulation;
KW transgenic plant; gene therapy; ss.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
FT CDS 56..1820
FT /*tag= a
FT /product= "protein phosphatase 2A regulatory
FT subunit A"
XX
PN WO200036121-A2.
XX
PD 22-JUN-2000.
XX
PF 15-DEC-1999; 99WO-US29823.
XX

PR 16-DEC-1998; 98US-0112541.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Famodu OO, Miao G, Sakai H, Lee J, Rafalski JA, Klein TM;
XX
DR WPI; 2000-431599/37.
DR P-PSDB; AAY99819.
XX
PT Polynucleotides encoding plant protein phosphatase useful for
PT modulating reversible protein phosphorylation in plants -
XX
PS Claim 4; Page 53-54; 73pp; English.
XX
CC The present sequence encodes corn protein phosphatase 2A regulatory
CC subunit A. The sequence was identified in clone p0018.chsug10r:fis of a
CC cDNA library made from corn ear shoot. BLAST analysis showed that the
CC present sequence encodes protein phosphatase 2A regulatory subunit A.
CC The sequence may be used for the recombinant production of the protein
CC in vivo, e.g. via a gene therapy protocol, or in vitro, e.g. in
CC fermentation culture. The protein may then be used to modulate the
CC process of reversible protein phosphorylation in plants. It may be used
CC directly to supplement a plant's own production of the enzyme or to
CC rectify mutations that result in the expression of inactive protein.
CC The protein may also be used to test for modulators of protein
CC phosphorylation which may be used to alter the activity of the enzyme.
XX
SQ Sequence 2061 BP; 549 A; 432 C; 498 G; 582 T; 0 other;

Query Match 51.5%; Score 121; DB 21; Length 2061;
Best Local Similarity 100.0%; Pred. No. 2.8e-31;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 GTTTTCCGTCTAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1908 GTTTTCCGTCTAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCC 1967

Qy      61 TGATCCATTGTTCGTTGTGTTATTAATGTTGTATAATTGAGCAGGACACAACACGTACGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1968 TGATCCATTGTTCGTTGTGTTATTAATGTTGTATAATTGAGCAGGACACAACACGTACGT 2027

Qy     121 T 121
           |
Db    2028 T 2028
```

RESULT 2
AAC47744
ID AAC47744 standard; DNA; 1674 BP.
XX
AC AAC47744;
XX
DT 18-OCT-2000 (first entry)
XX
DE Zea mays DNA fragment SEQ ID NO: 54954.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic;
KW pathway; promoter; termination sequence; corn; ss.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
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PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
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PR 28-JUN-1999; 99US-0140823.
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PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
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PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 29-OCT-1999; 99US-0162142.

Query Match 32.2%; Score 75.6; DB 21; Length 1674;
Best Local Similarity 65.5%; Pred. No. 1.1e-15;
Matches 78; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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Qy    117 ACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGGTTCATCAAGACCGC 176
          | |                                          ||||||||||||||||||
Db   1145 AGGGATGGTCACCATCAACCTCGACCTCAAGAAGGGCGGCAACAGGTTCATCAAGACCGC 1204

Qy    177 CGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTCAAGCCCC 235
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   1205 CGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGGGAGGTGGTCAAGCCCC 1263
```

RESULT 3
AAX07185
ID AAX07185 standard; cDNA; 1380 BP.
XX
AC AAX07185;
XX
DT 21-MAY-1999 (first entry)
XX
DE Wheat S-adenosylmethionine synthetase cDNA contig.
XX
KW S-adenosylmethionine synthetase; wheat; amino acid; lysine;
KW threonine; methionine; cysteine; isoleucine; transgenic plant;
KW crop improvement; food; feedstuff; ss.
XX
OS Triticum aestivum.
XX
FH Key Location/Qualifiers
FT CDS 73..1257
FT /*tag= a
XX
PN WO9855601-A2.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US11692.
XX
PR 12-JUN-1997; 97US-0049443.
PR 06-JUN-1997; 97US-0048771.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX
PI Abell LM, Allen SM, Falco SC, Hitz WD, Kinney AJ;
PI Rafalski JA, Thorpe CJ;
XX
DR WPI; 1999-070263/06.
DR P-PSDB; AAW97744.
XX
PT New plant amino acid biosynthetic enzymes, DNA and chimeric genes -
PT encode: dihydropicolinate reductase; diaminopimelate epimerase;
PT threonine synthase; threonine deaminase; S-adenosylmethionine
PT synthetase
XX
PS Claim 47; Page 69-70; 98pp; English.
XX
CC This is the nucleotide sequence of a cDNA contig that codes for
CC a full-length wheat S-adenosylmethionine synthetase (see AAW97744).
CC The contig was assembled from clones isolated from wheat kernel,
CC leaf, seedling and root cDNA libraries and identified by comparison
CC to public sequence databases using BLAST algorithms. It shows
CC sequence similarity to the barley enzyme. The invention relates to
CC new isolated nucleic acid fragments (see AAX07168-85) encoding plant
CC enzymes (see AAW97727-44) that catalyse steps in the biosynthesis of
CC lysine, threonine, methionine, cysteine and isoleucine from
CC aspartate, the enzyme being selected from dihydropicolinate reductase,
CC diaminopimelate epimerase, threonine synthase, threonine deaminase
CC or S-adenosylmethionine synthetase. The invention also relates to
CC the construction of a chimeric gene encoding all or a portion of
CC the biosynthetic pathway enzyme, in sense or antisense orientation,
CC where expression of the chimeric gene results in production of
CC altered levels of the enzyme in a transformed host cell.
CC Overexpression or reduction of expression of genes encoding the
CC amino acid biosynthetic pathway enzymes in crop plants such as
CC corn, soybean and wheat can be used to alter levels of the amino
CC acids in human food and animal feed. Transformed host cells can
CC also be used to identify compounds that inhibit one of the enzymes.
XX
SQ Sequence 1380 BP; 299 A; 430 C; 379 G; 267 T; 5 other;

Query Match 28.0%; Score 65.8; DB 20; Length 1380;
Best Local Similarity 90.9%; Pred. No. 2.4e-12;
Matches 70; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 159 CAGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTG 218
||||||||||||||||||| || ||||| |||||||||||||| || |||||||||||||
Db 1155 CAGGTTCATCAAGACCGCTGCTTACGGTCACTTTGGCCGTGATGATGCCGACTTCACCTG 1214

Qy 219 CGAGGTGGTCAAGCCCC 235
|||||||| |||||||
Db 1215 GGAGGTGGTGAAGCCCC 1231

RESULT 4
AAT99143
ID AAT99143 standard; cDNA to mRNA; 1182 BP.
XX
AC AAT99143;
XX
DT 26-MAR-1998 (first entry)
XX
DE S-adenosylmethionine synthase 3 gene.
XX
KW S-adenosylmethionine synthase 3 gene; barley; alkali resistant plant;
KW sam3; ss.
XX
OS Hordeum vulgare.
XX
PN JP09313186-A.
XX
PD 09-DEC-1997.
XX
PF 28-MAY-1996; 96JP-0133406.
XX
PR 28-MAY-1996; 96JP-0133406.
XX
PA (NIOC) NIPPON OIL CO LTD.
XX
DR WPI; 1998-080077/08.
DR P-PSDB; AAW34542.
XX
PT S-adenosyl-methionine synthase gene - useful in producing plants
PT resistant to alkaline soil
XX
PS Claim 6; Page 10-11; 13pp; Japanese.
XX
CC This sequence represents the S-adenosylmethionine synthase 3 (sam3)
CC gene. This DNA sequence may be used in a vector to produce plants which
CC are resistant to alkaline soil.
XX
SQ Sequence 1182 BP; 253 A; 368 C; 331 G; 230 T; 0 other;

Query Match 26.2%; Score 61.6; DB 19; Length 1182;
Best Local Similarity 88.2%; Pred. No. 6.3e-11;
Matches 67; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 160 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 219
||||||||||||||| || || || || |||||||||| ||||| ||||||||||||||
Db 1084 AGGTTCATCAAGACAGCTGCTTATGGTCACTTTGGCCGCGACGATGCCGACTTCACCTGG 1143

Qy 220 GAGGTGGTCAAGCCCC 235
|||||||| |||||||
Db 1144 GAGGTGGTGAAGCCCC 1159

RESULT 5
AAT99141
ID AAT99141 standard; cDNA to mRNA; 1182 BP.
XX
AC AAT99141;
XX
DT 26-MAR-1998 (first entry)
XX
DE S-adenosylmethionine synthase 1 gene.
XX
KW S-adenosylmethionine synthase 1 gene; barley; alkali resistant plant;
KW sam1; ss.
XX
OS Hordeum vulgare.
XX
PN JP09313186-A.
XX
PD 09-DEC-1997.
XX
PF 28-MAY-1996; 96JP-0133406.
XX
PR 28-MAY-1996; 96JP-0133406.
XX
PA (NIOC) NIPPON OIL CO LTD.
XX
DR WPI; 1998-080077/08.
DR P-PSDB; AAW34540.
XX
PT S-adenosyl-methionine synthase gene - useful in producing plants
PT resistant to alkaline soil
XX
PS Claim 4; Page 8-9; 13pp; Japanese.
XX
CC This sequence represents the S-adenosylmethionine synthase 1 (sam1)
CC gene. This DNA sequence may be used in a vector to produce plants which
CC are resistant to alkaline soil.
XX
SQ Sequence 1182 BP; 253 A; 372 C; 324 G; 233 T; 0 other;

Query Match 26.0%; Score 61; DB 19; Length 1182;
Best Local Similarity 87.0%; Pred. No. 1e-10;
Matches 67; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```
Qy     159 CAGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTG 218
           ||||||||||||||| || || ||||| |||||||||| || || || ||||||||||
Db    1083 CAGGTTCATCAAGACAGCTGCTTACGGTCACTTTGGCCGCGATGATGCTGACTTCACCTG 1142

Qy     219 CGAGGTGGTCAAGCCCC 235
           |||||||| |||||||
Db    1143 GGAGGTGGTGAAGCCCC 1159


RESULT 6
AAT99142
ID   AAT99142 standard; cDNA to mRNA; 1182 BP.
XX
AC   AAT99142;
XX
DT   26-MAR-1998  (first entry)
XX
DE   S-adenosylmethionine synthase 2 gene.
XX
KW   S-adenosylmethionine synthase 2 gene; barley; alkali resistant plant;
KW   sam2; ss.
XX
OS   Hordeum vulgare.
XX
PN   JP09313186-A.
XX
PD   09-DEC-1997.
XX
PF   28-MAY-1996;   96JP-0133406.
XX
PR   28-MAY-1996;   96JP-0133406.
XX
PA   (NIOC ) NIPPON OIL CO LTD.
XX
DR   WPI; 1998-080077/08.
DR   P-PSDB; AAW34541.
XX
PT   S-adenosyl-methionine synthase gene - useful in producing plants
PT   resistant to alkaline soil
XX
PS   Claim 5; Page 9-10; 13pp; Japanese.
XX
CC   This sequence represents the S-adenosylmethionine synthase 2 (sam2)
CC   gene. This DNA sequence may be used in a vector to produce plants which
CC   are resistant to alkaline soil.
XX
SQ   Sequence 1182 BP; 261 A; 368 C; 324 G; 229 T; 0 other;

  Query Match             25.3%;  Score 59.4;  DB 19;  Length 1182;
  Best Local Similarity   85.7%;  Pred. No. 3.6e-10;
  Matches   66;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy     159 CAGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTG 218
           ||||||||||||||| || || ||||| ||||| ||||| || || || ||||||||||
Db    1083 CAGGTTCATCAAGACAGCTGCTTACGGTCACTTCGGCCGCGATGATGCTGACTTCACCTG 1142

Qy     219 CGAGGTGGTCAAGCCCC 235
           |||||||| |||||||
Db    1143 GGAGGTGGTGAAGCCCC 1159


RESULT 7
AAX81128
ID   AAX81128 standard; cDNA; 399 BP.
XX
AC   AAX81128;
XX
DT   06-SEP-1999  (first entry)
XX
DE   S-adenosyl methionine (SAM) partial cDNA sequence.
XX
KW   Senescence-associated receptor-like protein kinase; sark; sam gene; sag;
KW   senescence-associated gene; plant senescence; promoter; pharmaceutical;
KW   plant maturation; S-adenosyl methionine; flower; fruit development; ss.
XX
OS   Phaseolus vulgaris.
XX
PN   WO9929159-A1.
XX
PD   17-JUN-1999.
XX
PF   08-DEC-1998;   98WO-US25799.
XX
PR   08-DEC-1997;   97US-0067898.
XX
PA   (VITA-) VITALITY BIOTECHNOLOGIES INC.
XX
PI   Gepstein S,  Hajuoje T,  Rosner A;
XX
DR   WPI; 1999-404873/34.
DR   P-PSDB; AAY21978.
XX
PT   DNA encoding senescence-associated genes for a senescence
PT   receptor-like protein kinase
XX
PS   Claim 18; Fig 4; 70pp; English.
XX
CC   The invention relates to a senescence-associated receptor-like protein
CC   kinase (sark) gene. The sark gene is a senescence-associated gene (sag)
CC   and is expressed early in the plant senescence process. The sark gene
CC   promoter is useful for driving expression of foreign genes having a
CC   desired product, such as a pharmaceutical, during the process of plant
CC   maturation. The sark gene promoter can be used to drive expression of
CC   resistance genes against pathogens or pests during senescence when the
CC   plant is particularly susceptible to infection or infestation. The sark
CC   gene promoter may also be used to drive expression of a gene encoding an
CC   inhibitor of senescence. Plant senescence may be inhibited by use of
CC   antisense sark constructs. Over expression of the sag genes, using the
CC   sark or sam (S-adenosyl methionine) gene promoters is useful for
CC   induction of early senescence. This is useful to obtain flower or fruit
CC   development prior to specific pest onset, prior to undesirable cross-
CC   fertilization from related crops, at a specific time during storage or
CC   retail, or to avoid development of plant structures that are not of
CC   agronomic importance. The present sequence represents a partial cDNA
CC   clone of S-adenosyl methionine (SAM).
XX
SQ   Sequence 399 BP; 108 A; 80 C; 82 G; 129 T; 0 other;

  Query Match             23.2%;  Score 54.6;  DB 20;  Length 399;
  Best Local Similarity   81.8%;  Pred. No. 1e-08;
  Matches   63;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy     159 CAGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTG 218
           ||||||| | ||||| || ||||| || ||||| ||| | || ||||| |||||||| ||
Db     101 CAGGTTCTTGAAGACTGCTGCATATGGACACTTCGGCAGAGAGGACGCTGACTTCACATG 160

Qy     219 CGAGGTGGTCAAGCCCC 235
           || ||||||||||||||
Db     161 GGAAGTGGTCAAGCCCC 177


RESULT 8
AAX07184
ID   AAX07184 standard; cDNA; 1485 BP.
XX
AC   AAX07184;
XX
DT   21-MAY-1999  (first entry)
XX
DE   Soybean S-adenosylmethionine synthetase cDNA clone s2.12b06.
XX
KW   S-adenosylmethionine synthetase; soybean; amino acid; lysine;
KW   threonine; methionine; cysteine; isoleucine; transgenic plant;
KW   crop improvement; food; feedstuff; ss.
XX
OS   Glycine max.
```

```
XX
FH   Key             Location/Qualifiers
FT   CDS             74..1252
FT                   /*tag=  a
XX
PN   WO9855601-A2.
XX
PD   10-DEC-1998.
XX
PF   05-JUN-1998;   98WO-US11692.
XX
PR   12-JUN-1997;   97US-0049443.
PR   06-JUN-1997;   97US-0048771.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Abell LM,  Allen SM,  Falco SC,  Hitz WD,  Kinney AJ;
PI   Rafalski JA,  Thorpe CJ;
XX
DR   WPI; 1999-070263/06.
DR   P-PSDB; AAW97743.
XX
PT   New plant amino acid biosynthetic enzymes, DNA and chimeric genes -
PT   encode: dihydropicolinate reductase; diaminopimelate epimerase;
PT   threonine synthase; threonine deaminase; S-adenosylmethionine
PT   synthetase
XX
PS   Claim 44; Page 66-67; 98pp; English.
XX
CC   This is the nucleotide sequence of cDNA clone s2.12b06, which
CC   codes for a full-length soybean S-adenosylmethionine synthetase
CC   (see AAW97743). The clone was isolated from a soybean seed cDNA
CC   library and identified by comparison to public sequence databases
CC   using BLAST algorithms. It shows sequence similarity to the
CC   tomato enzyme. The invention relates to new isolated nucleic
CC   acid fragments (see AAX07168-85) encoding plant enzymes (see
CC   AAW97727-44) that catalyse steps in the biosynthesis of lysine,
CC   threonine, methionine, cysteine and isoleucine from aspartate, the
CC   enzyme being selected from dihydropicolinate reductase,
CC   diaminopimelate epimerase, threonine synthase, threonine deaminase
CC   or S-adenosylmethionine synthetase. The invention also relates to
CC   the construction of a chimeric gene encoding all or a portion of
CC   the biosynthetic pathway enzyme, in sense or antisense orientation,
CC   where expression of the chimeric gene results in production of
CC   altered levels of the enzyme in a transformed host cell.
CC   Overexpression or reduction of expression of genes encoding the
CC   amino acid biosynthetic pathway enzymes in crop plants such as
CC   corn, soybean and wheat can be used to alter levels of the amino
CC   acids in human food and animal feed. Transformed host cells can
CC   also be used to identify compounds that inhibit one of the enzymes.
XX
SQ   Sequence 1485 BP; 366 A; 373 C; 357 G; 389 T; 0 other;

  Query Match             22.6%;  Score 53;  DB 20;  Length 1485;
  Best Local Similarity   80.5%;  Pred. No. 6.4e-08;
  Matches   62;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy     159 CAGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTG 218
           ||||||| | ||||| || ||||| || ||||| ||| | || ||| | |||||||| ||
Db    1156 CAGGTTCTTGAAGACTGCTGCATATGGACACTTCGGCAGAGAGGACCCTGACTTCACATG 1215

Qy     219 CGAGGTGGTCAAGCCCC 235
             || ||||||||||||||
Db    1216 GGAAGTGGTCAAGCCCC 1232


RESULT 9
AAA51037
ID   AAA51037 standard; cDNA; 1518 BP.
XX
AC   AAA51037;
XX
DT   09-OCT-2000  (first entry)
XX
DE   Soybean S-adenosyl-L-methionine synthetase cDNA.
XX
KW   S-adenosyl-L-methionine synthetase; SAMS; probe; promoter; embryo;
KW   constitutive; tissue-specific; development-specific;
KW   herbicide resistance; pathogen resistance; ss.
XX
OS   Glycine max.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..73
FT                   /*tag=  a
FT   CDS             74..1252
FT                   /*tag=  b
FT                   /product= S-adenosyl-L-methionine_Synthetase
XX
PN   WO200037662-A2.
XX
PD   29-JUN-2000.
XX
PF   17-DEC-1999;   99WO-US30180.
XX
PR   21-DEC-1998;   98US-0113045.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Falco SC,  Li Z;
XX
DR   WPI; 2000-442682/38.
XX
PT   S-adenosyl-L-methionine synthetase promoter for expressing target
PT   heterologous herbicide-resistance or pathogen-resistance nucleic acid
PT   fragments in plants, especially soybean
XX
PS   Example 2; Page 39; 50pp; English.
XX
CC   This is the soybean full-length S-adenosyl-L-methionine synthetase (SAMS)
CC   cDNA, which was used to generate a probe to isolate a SAMS promoter. The
CC   SAMS promoter is active in seedlings and callus and over-expression of a
CC   gene in embryo stage can be achieved at an early developing stage using
CC   the SAMS promoter. The SAMS promoter may be used as an alternative to
CC   cauliflower mosaic virus 35S promoter to drive expression of selectable
CC   marker genes. Plant cells transformed with the SAMS constitutive promoter
CC   are useful for increasing or decreasing the expression of heterologous
CC   nucleic acid fragments in a plant, preferably corn, rice, wheat, barley,
CC   palm, Arabidopsis, soybean, oil seed Brassica, peanut, sunflower,
CC   safflower, cotton, tobacco, tomato, potato or cocoa. Target heterologous
CC   nucleic acid fragments include herbicide or pathogen resistance
CC   nucleic acid fragments.
XX
SQ   Sequence 1518 BP; 399 A; 373 C; 357 G; 389 T; 0 other;

  Query Match             22.6%;  Score 53;  DB 21;  Length 1518;
  Best Local Similarity   80.5%;  Pred. No. 6.5e-08;
  Matches   62;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy     159 CAGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTG 218
           ||||||| | ||||| || ||||| || ||||| ||| | || ||| | |||||||| ||
Db    1156 CAGGTTCTTGAAGACTGCTGCATATGGACACTTCGGCAGAGAGGACCCTGACTTCACATG 1215

Qy     219 CGAGGTGGTCAAGCCCC 235
             || ||||||||||||||
Db    1216 GGAAGTGGTCAAGCCCC 1232


RESULT 10
AAX07183
ID   AAX07183 standard; cDNA; 1582 BP.
XX
AC   AAX07183;
XX
DT   21-MAY-1999  (first entry)
XX
```

```
DE   Corn S-adenosylmethionine synthetase cDNA clone cc3.mn0002.d2.
XX
KW   S-adenosylmethionine synthetase; corn; maize; amino acid; lysine;
KW   threonine; methionine; cysteine; isoleucine; transgenic plant;
KW   crop improvement; food; feedstuff; ss.
XX
OS   Zea mays.
XX
FH   Key             Location/Qualifiers
FT   CDS             140..1330
FT                   /*tag= a
XX
PN   WO9855601-A2.
XX
PD   10-DEC-1998.
XX
PF   05-JUN-1998;    98WO-US11692.
XX
PR   12-JUN-1997;    97US-0049443.
PR   06-JUN-1997;    97US-0048771.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Abell LM,  Allen SM,  Falco SC,  Hitz WD,  Kinney AJ;
PI   Rafalski JA,  Thorpe CJ;
XX
DR   WPI; 1999-070263/06.
DR   P-PSDB; AAW97742.
XX
PT   New plant amino acid biosynthetic enzymes, DNA and chimeric genes -
PT   encode: dihydropicolinate reductase; diaminopimelate epimerase;
PT   threonine synthase; threonine deaminase; S-adenosylmethionine
PT   synthetase
XX
PS   Claim 41; Page 62-63; 98pp; English.
XX
CC   This is the nucleotide sequence of cDNA clone cc3.mn0002.d2, which
CC   codes for a full-length corn S-adenosylmethionine synthetase
CC   (see AAW97742). The clone was isolated from a corn callus cDNA
CC   library and identified by comparison to public sequence databases
CC   using BLAST algorithms. It shows sequence similarity to the
CC   Oryza sativa enzyme. The invention relates to new isolated
CC   nucleic acid fragments (see AAX07168-85) encoding plant enzymes (see
CC   AAW97727-44) that catalyse steps in the biosynthesis of lysine,
CC   threonine, methionine, cysteine and isoleucine from aspartate, the
CC   enzyme being selected from dihydropicolinate reductase,
CC   diaminopimelate epimerase, threonine synthase, threonine deaminase
CC   or S-adenosylmethionine synthetase. The invention also relates to
CC   the construction of a chimeric gene encoding all or a portion of
CC   the biosynthetic pathway enzyme, in sense or antisense orientation,
CC   where expression of the chimeric gene results in production of
CC   altered levels of the enzyme in a transformed host cell.
CC   Overexpression or reduction of expression of genes encoding the
CC   amino acid biosynthetic pathway enzymes in crop plants such as
CC   corn, soybean and wheat can be used to alter levels of the amino
CC   acids in human food and animal feed. Transformed host cells can
CC   also be used to identify compounds that inhibit one of the enzymes.
XX
SQ   Sequence 1582 BP; 340 A; 474 C;'417 G; 351 T; 0 other;

  Query Match             21.7%;  Score 51;  DB 20;  Length 1582;
  Best Local Similarity   80.0%;  Pred. No. 3.2e-07;
  Matches   60;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy     161 GGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCG 220
           | | | |||||||  || ||  ||||||||||||  ||   | ||||||  | ||||||||||| |
Db    1230 GCTACCTCAAGACGGCAGCCTACGGCCACTTCGGAAGGGACGACCCTGACTTCACCTGGG 1289

Qy     221 AGGTGGTCAAGCCCC 235
           ||||||| |||||  |
Db    1290 AGGTGGTGAAGCCAC 1304
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RESULT 11
AAC44219
ID   AAC44219 standard; DNA; 635 BP.
XX
AC   AAC44219;
XX
DT   18-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana DNA fragment SEQ ID NO: 42062.
XX
KW   Hybridisation assay; genetic mapping; gene expression control;
KW   protein identification; signal transduction pathway;
KW   metabolic pathway; promoter; termination sequence; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;   99US-0121825.
PR   05-MAR-1999;   99US-0123180.
PR   09-MAR-1999;   99US-0123548.
PR   23-MAR-1999;   99US-0125788.
PR   25-MAR-1999;   99US-0126264.
PR   29-MAR-1999;   99US-0126785.
PR   01-APR-1999;   99US-0127462.
PR   06-APR-1999;   99US-0128234.
PR   08-APR-1999;   99US-0128714.
PR   16-APR-1999;   99US-0129845.
PR   19-APR-1999;   99US-0130077.
PR   21-APR-1999;   99US-0130449.
PR   23-APR-1999;   99US-0130510.
PR   23-APR-1999;   99US-0130891.
PR   28-APR-1999;   99US-0131449.
PR   30-APR-1999;   99US-0132048.
PR   30-APR-1999;   99US-0132407.
PR   04-MAY-1999;   99US-0132484.
PR   05-MAY-1999;   99US-0132485.
PR   06-MAY-1999;   99US-0132486.
PR   06-MAY-1999;   99US-0132487.
PR   07-MAY-1999;   99US-0132863.
PR   11-MAY-1999;   99US-0134256.
PR   14-MAY-1999;   99US-0134218.
PR   14-MAY-1999;   99US-0134219.
PR   14-MAY-1999;   99US-0134221.
PR   14-MAY-1999;   99US-0134370.
PR   18-MAY-1999;   99US-0134768.
PR   19-MAY-1999;   99US-0134941.
PR   20-MAY-1999;   99US-0135124.
PR   21-MAY-1999;   99US-0135353.
PR   24-MAY-1999;   99US-0135629.
PR   25-MAY-1999;   99US-0136021.
PR   27-MAY-1999;   99US-0136392.
PR   28-MAY-1999;   99US-0136782.
PR   01-JUN-1999;   99US-0137222.
PR   03-JUN-1999;   99US-0137528.
PR   04-JUN-1999;   99US-0137502.
PR   07-JUN-1999;   99US-0137724.
PR   08-JUN-1999;   99US-0138094.
PR   10-JUN-1999;   99US-0138540.
PR   10-JUN-1999;   99US-0138847.
PR   14-JUN-1999;   99US-0139119.
PR   16-JUN-1999;   99US-0139452.
PR   16-JUN-1999;   99US-0139453.
PR   17-JUN-1999;   99US-0139492.
PR   18-JUN-1999;   99US-0139454.
PR   18-JUN-1999;   99US-0139455.
PR   18-JUN-1999;   99US-0139456.
PR   18-JUN-1999;   99US-0139457.
PR   18-JUN-1999;   99US-0139458.
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PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
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Query Match 21.4%; Score 50.4; DB 21; Length 635;
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KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
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Query Match 21.4%; Score 50.4; DB 21; Length 1508;
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AC AAC45478;
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DT 18-OCT-2000 (first entry)
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
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Query Match 21.4%; Score 50.4; DB 21; Length 1521;
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KW metabolic pathway; promoter; termination sequence; ss.
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
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XX
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.

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PR 13-AUG-1999; 99US-0148684.
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PR   28-SEP-1999;   99US-0156458.
PR   29-SEP-1999;   99US-0156596.
PR   04-OCT-1999;   99US-0157117.
PR   05-OCT-1999;   99US-0157753.
PR   06-OCT-1999;   99US-0157865.
PR   07-OCT-1999;   99US-0158029.
PR   08-OCT-1999;   99US-0158232.
PR   12-OCT-1999;   99US-0158369.
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PR   28-OCT-1999;   99US-0161992.
PR   28-OCT-1999;   99US-0161993.
PR   29-OCT-1999;   99US-0162142.

  Query Match             21.2%;  Score 49.8;  DB 21;  Length 1654;
  Best Local Similarity   77.9%;  Pred. No. 8.5e-07;
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Qy     159 CAGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTG 218
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Db    1228 CAGGTTCCAGAAAACCGCTGCGTATGGCCATTTCGGGCGTGATGACCCTGACTTCACTTG 1287

Qy     219 CGAGGTGGTCAAGCCCC 235
           ||||| |||||||| |
Db    1288 GGAGGTTGTCAAGCCGC 1304


RESULT 17
AAD02296
ID   AAD02296 standard; DNA; 1636 BP.
XX
AC   AAD02296;
XX
DT   28-MAR-2001  (first entry)
XX
DE   Nicotiana tabacum S-adenosylmethionine synthetase (SAMS) DNA.
XX
KW   Tobacco; alkaloid; nicotine; transgenic plant; pharmaceutical protein;
KW   herbicide resistance; S-adenosylmethionine synthetase; SAMS; ds.
XX
OS   Nicotiana tabacum.
XX
FH   Key             Location/Qualifiers
FT   CDS             96..1268
FT                   /*tag=  a
FT                   /product= "Nicotiana tabacum S-adenosylmethionine
FT                   synthetase (SAMS) protein"
XX
PN   WO200067558-A1.
XX
PD   16-NOV-2000.
XX
PF   05-MAY-2000; 2000WO-US12450.
XX
PR   06-MAY-1999;   99US-0132919.
XX
PA   (TIMK/) TIMKO M.
XX
PI   Timko M;
XX
DR   WPI; 2001-007279/01.
DR   P-PSDB; AAY72078.
XX
PT   New nucleic acid encoding alkaloid-synthesis enzymes in tobacco, useful
PT   e.g. for producing transgenic plants with altered nicotine content -
XX
PS   Claim 1; Page 78-79; 103pp; English.
XX
CC   The invention relates to enzymes involved in alkaloid, specifically
CC   nicotine, synthesis in tobacco and nucleic acids encoding them. The
CC   nucleic acid of the invention can be used, in sense or antisense
CC   orientation, to produce transgenic tobacco plants with altered
CC   alkaloid content, and also for expression of exogenous proteins,
CC   e.g. pharmaceutical proteins or proteins implicated in resistance
CC   to herbicides. The protein of the invention can be used to
CC   identify modulators of enzymatic activity in plants.
CC   The present sequence is Nicotiana tabacum S-adenosylmethionine
CC   synthetase (SAMS) DNA. This enzyme is involved in the nicotine
CC   biosynthetic pathway.
XX
SQ   Sequence 1636 BP; 444 A; 365 C; 373 G; 454 T; 0 other;

  Query Match             19.8%;  Score 46.6;  DB 22;  Length 1636;
  Best Local Similarity   75.3%;  Pred. No. 1.1e-05;
  Matches   58;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy     159 CAGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTG 218
           ||||| |   ||||| || || || || |||||||||||||| ||| |||||||| | ||
Db    1175 CAGGTACCAGAAGACTGCAGCTTATGGTCACTTTGGCCGTGATGACCCCGACTTCTCATG 1234

Qy     219 CGAGGTGGTCAAGCCCC 235
             |||   ||||||  ||
Db    1235 GGAGACTGTCAAGGTCC 1251


RESULT 18
AAC46421
ID   AAC46421 standard; DNA; 1393 BP.
XX
AC   AAC46421;
XX
DT   18-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana DNA fragment SEQ ID NO: 50076.
XX
KW   Hybridisation assay; genetic mapping; gene expression control;
KW   protein identification; signal transduction pathway;
KW   metabolic pathway; promoter; termination sequence; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;   99US-0121825.
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PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
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PR 28-OCT-1999; 99US-0161992.
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Query Match 18.0%; Score 42.4; DB 21; Length 1393;
Best Local Similarity 72.4%; Pred. No. 0.00028;
Matches 55; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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Db    1175 AGGTTTCAGAAAACGGCAGCGTATGGACATTTCGGAAGAGACGACCCTGACTTCACCTGG 1234

Qy     220 GAGGTGGTCAAGCCCC 235
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Db    1235 GAGGTCGTGAAGCCAC 1250
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RESULT 19
AAC33674
ID AAC33674 standard; DNA; 1395 BP.
XX
AC AAC33674;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 3906.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
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PR 25-MAR-1999; 99US-0126264.
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PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 18.0%; Score 42.4; DB 21; Length 1395;
Best Local Similarity 72.4%; Pred. No. 0.00028;
Matches 55; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

```
Qy    160 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 219
          |||||    || || || || || || || || ||  | |||||| | ||||||||||
Db   1175 AGGTTTCAGAAAACGGCAGCGTATGGACATTTCGGAAGAGACGACCCTGACTTCACCTGG 1234

Qy    220 GAGGTGGTCAAGCCCC 235
          ||||| || ||||| |
Db   1235 GAGGTCGTGAAGCCAC 1250
```

RESULT 20
AAQ64204
ID AAQ64204 standard; cDNA; 1208 BP.
XX
AC AAQ64204;
XX
DT 18-NOV-1994 (first entry)
XX
DE snaC gene encoding enzyme in streptogramin biosynthetic pathway.
XX
KW Antibiotic; streptogramin; snaA; snaB; snaC; biosynthesis; enzyme;
KW biosynthetic pathway; Streptomyces pristinaespiralis; ds.
XX
OS Streptomyces pristinaespiralis.
XX
FH Key Location/Qualifiers
FT CDS 1..1209
FT /*tag= a
XX
PN FR2696189-A.
XX
PD 01-APR-1994.
XX
PF 25-SEP-1992; 92FR-0011441.
XX
PR 25-SEP-1992; 92FR-0011441.
XX
PA (RHON) RHONE POULENC RORER SA.
XX

```
PI   Blanc V,  Blanche F,  Crouzet J,  Jacques N,  Lacroix P;
PI   Thibaut D,  Zagorec M;
XX
DR   WPI; 1994-128286/16.
DR   P-PSDB; AAR54204.
XX
PT   DNA involved in streptogramin antibiotic biosynthesis - for
PT   prodn. or bio-conversion of streptogramin(s) or prodn. of
PT   streptogramin intermediates, derivs. or hybrid antibiotics
XX
PS   Claim 2; Page 54-55; 83pp; French.
XX
CC   The snaC gene product is involved in the biosynthesis of
CC   streptogramins, antibiotics active against Gram-positive bacteria.
CC   The identification of the sequences encoding the enzymes involved
CC   in the biosynthetic pathway means that they can be isolated and
CC   manipulated.  Mutant microorganisms in which a step in the
CC   streptogramin biosynthetic pathway is blocked can be cultured to
CC   produce streptogramin intermediates, which may later be converted
CC   to streptogramin derivatives.  Recombinant cells may also be used
CC   for the bioconversion of streptogramins from one form to another or
CC   for the production of hybrid antibiotics.
XX
SQ   Sequence 1208 BP; 190 A; 500 C; 360 G; 158 T; 0 other;

  Query Match             17.1%;  Score 40.2;  DB 15;  Length 1208;
  Best Local Similarity   46.7%;  Pred. No. 0.0015;
  Matches   57;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy     113 ACGTACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGGTTCATCAAGA 172
           || | ||                                              ||  | |  |   |
Db    1055 ACCTGCGCCCCGCGGCCATCATCCGCGACCTCGACCTGCTGCGGCCCATCTACGCCGCCA 1114

Qy     173 CCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTCAAGC 232
           ||||||| |||||||||||| ||||| ||     |||||||||||| |||  |  | | |
Db    1115 CCGCCGCCTACGGCCACTTCGGCCGCGAACTGCCCGACTTCACCTGGGAGCGGACCGACC 1174

Qy     233 CC 234
           |
Db    1175 GC 1176


RESULT 21
AAQ64201
ID   AAQ64201 standard; cDNA; 5392 BP.
XX
AC   AAQ64201;
XX
DT   18-NOV-1994  (first entry)
XX
DE   Sequence comprising the snaA, snaB and snaC gene cluster.
XX
KW   Antibiotic; streptogramin; snaA; snaB; snaC; biosynthesis; enzyme;
KW   biosynthetic pathway; Streptomyces pristinaespiralis; ds.
XX
OS   Streptomyces pristinaespiralis.
XX
PN   FR2696189-A.
XX
PD   01-APR-1994.
XX
PF   25-SEP-1992;   92FR-0011441.
XX
PR   25-SEP-1992;   92FR-0011441.
XX
PA   (RHON ) RHONE POULENC RORER SA.
XX
PI   Blanc V,  Blanche F,  Crouzet J,  Jacques N,  Lacroix P;
PI   Thibaut D,  Zagorec M;
XX
DR   WPI; 1994-128286/16.
XX
PT   DNA involved in streptogramin antibiotic biosynthesis - for
PT   prodn. or bio-conversion of streptogramin(s) or prodn. of
PT   streptogramin intermediates, derivs. or hybrid antibiotics
XX
PS   Disclosure; Page 44-47; 83pp; French.
XX
CC   This sequence comprises the snaA, snaB and snaC genes which are
CC   involved in the biosynthesis of streptogramins, antibiotics active
CC   against Gram-positive bacteria.  The identification of the sequences
CC   encoding the enzymes involved in the biosynthetic pathway means that
CC   they can be isolated and manipulated.  Mutant microorganisms in
CC   which a step in the streptogramin biosynthetic pathway is blocked
CC   can be cultured to produce streptogramin intermediates, which may
CC   later be converted to streptogramin derivatives.  Recombinant cells
CC   may also be used for the bioconversion of streptogramins from one
CC   form to another or for the production of hybrid antibiotics.
XX
SQ   Sequence 5392 BP; 811 A; 2161 C; 1671 G; 749 T; 0 other;

  Query Match             17.1%;  Score 40.2;  DB 15;  Length 5392;
  Best Local Similarity   46.7%;  Pred. No. 0.0029;
  Matches   57;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy     113 ACGTACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGGTTCATCAAGA 172
           || | ||                                              ||  | |  |   |
Db    4612 ACCTGCGCCCCGCGGCCATCATCCGCGACCTCGACCTGCTGCGGCCCATCTACGCCGCCA 4671

Qy     173 CCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTCAAGC 232
           ||||||| |||||||||||| ||||| ||     |||||||||||| |||  |  | | |
Db    4672 CCGCCGCCTACGGCCACTTCGGCCGCGAACTGCCCGACTTCACCTGGGAGCGGACCGACC 4731

Qy     233 CC 234
           |
Db    4732 GC 4733


RESULT 22
AAD22684
ID   AAD22684 standard; DNA; 4848 BP.
XX
AC   AAD22684;
XX
DT   26-FEB-2002  (first entry)
XX
DE   Streptomyces fradiae S-adenosylmethionine (SAM) operon DNA.
XX
KW   S-adenosylmethionine; SAM operon; SAM synthetase; methyltransferase;
KW   MT; methylene tetrahydrofolate reductase; MTHR; activated methyl cycle;
KW   tylosin production; ds.
XX
OS   Streptomyces fradiae.
XX
FH   Key             Location/Qualifiers
FT   CDS             986..2209
FT                   /*tag=  a
FT                   /product= "SAM synthetase protein"
FT   CDS             2241..3341
FT                   /*tag=  b
FT                   /product= "Methyltransferase protein"
FT                   /transl_except= (2241..2243, aa:Met)
FT   CDS             3338..4255
FT                   /*tag=  c
FT                   /product= "Methylene tetrahydrofolate reductase protein"
FT                   /transl_except= (3338..3340, aa:Met)
XX
PN   US6312920-B1.
XX
PD   06-NOV-2001.
XX
PF   22-OCT-1997;   97US-0955957.
XX
PR   13-NOV-1996;   96US-030898P.
XX
PA   (ELIL ) LILLY & CO ELI.
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XX
PI   DeHoff BS,  Rosteck PR;
XX
DR   WPI; 2002-024904/03.
DR   P-PSDB; AAE13583, AAE13584, AAE13585.
XX
PT   New S-adenosylmethionine (SAM) operon from Streptomyces fradiae which
PT   encodes SAM synthetase, methyltransferase and methylene
PT   tetrahydrofolate reductase, useful for producing SAM by recombinant
PT   techniques -
XX
PS   Claim 19; Column 11-20; 22pp; English.
XX
CC   The patent discloses Streptomyces fradiae S-adenosylmethionine (SAM)
CC   operon which comprises three genes encoding SAM synthetase, methyl-
CC   transferase (MT) and methylene tetrahydrofolate reductase (MTHR).
CC   SAM synthetase, MT and MTHR together comprise the activated methyl
CC   cycle which produces SAM and provides methyl groups required for
CC   the final steps in tylosin production. The invention also relates
CC   to vectors and transformed heterologous host cells for expressing
CC   SAM synthetase. It also relates to a method useful for producing
CC   SAM by recombinant techniques. The present DNA sequence is SAM
CC   operon from Streptomyces fradiae.
XX
SQ   Sequence 4848 BP; 648 A; 1869 C; 1696 G; 635 T; 0 other;

  Query Match             17.0%;  Score 40;  DB 24;  Length 4848;
  Best Local Similarity   47.7%;  Pred. No. 0.0032;
  Matches   52;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy     113 ACGTACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGGTTCATCAAGA 172
           || | ||                                          |  | |  |||||
Db    2055 ACCTCCGCCCGGCCGCGATCATCCGGGATCTGGACCTGCTCCGCCCGATCTACGCCAAGA 2114

Qy     173 CCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGA 221
           ||||||| |||||||||||| ||||| ||     |||| |||||||| ||
Db    2115 CCGCCGCCTACGGCCACTTCGGCCGCGAACTGCCCGAGTTCACCTGGGA 2163


RESULT 23
AAD22686
ID   AAD22686 standard; mRNA; 4848 BP.
XX
AC   AAD22686;
XX
DT   26-FEB-2002  (first entry)
XX
DE   Streptomyces fradiae S-adenosylmethionine (SAM) operon mRNA.
XX
KW   S-adenosylmethionine; SAM operon; SAM synthetase; methyltransferase;
KW   MT; methylene tetrahydrofolate reductase; MTHR; activated methyl cycle;
KW   tylosin production; ss.
XX
OS   Streptomyces fradiae.
XX
PN   US6312920-B1.
XX
PD   06-NOV-2001.
XX
PF   22-OCT-1997;   97US-0955957.
XX
PR   13-NOV-1996;   96US-030898P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   DeHoff BS,  Rosteck PR;
XX
DR   WPI; 2002-024904/03.
XX
PT   New S-adenosylmethionine (SAM) operon from Streptomyces fradiae which
PT   encodes SAM synthetase, methyltransferase and methylene
PT   tetrahydrofolate reductase, useful for producing SAM by recombinant
PT   techniques -
XX
PS   Claim 19; Column 31-36; 22pp; English.
XX
CC   The patent discloses Streptomyces fradiae S-adenosylmethionine (SAM)
CC   operon which comprises three genes encoding SAM synthetase, methyl-
CC   transferase (MT) and methylene tetrahydrofolate reductase (MTHR).
CC   SAM synthetase, MT and MTHR together comprise the activated methyl
CC   cycle which produces SAM and provides methyl groups required for
CC   the final steps in tylosin production. The invention also relates
CC   to vectors and transformed heterologous host cells for expressing
CC   SAM synthetase. It also relates to a method useful for producing
CC   SAM by recombinant techniques. The present mRNA sequence is SAM
CC   operon from Streptomyces fradiae.
XX
SQ   Sequence 4848 BP; 648 A; 1869 C; 1696 G; 635 U; 0 other;

  Query Match             17.0%;  Score 40;  DB 24;  Length 4848;
  Best Local Similarity   40.4%;  Pred. No. 0.0032;
  Matches   44;  Conservative    8;  Mismatches   57;  Indels    0;  Gaps    0;

Qy     113 ACGTACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGGTTCATCAAGA 172
           || : ||                                          |  : |  |||||
Db    2055 ACCUCCGCCCGGCCGCGAUCAUCCGGGAUCUGGACCUGCUCCGCCCGAUCUACGCCAAGA 2114

Qy     173 CCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGA 221
           ||||||| :|||||||:: ||||| ||     |||| ::||||:|| ||
Db    2115 CCGCCGCCUACGGCCACUUCGGCCGCGAACUGCCCGAGUUCACCUGGGA 2163


RESULT 24
AAA75637/c
ID   AAA75637 standard; DNA; 1693 BP.
XX
AC   AAA75637;
XX
DT   22-JAN-2001  (first entry)
XX
DE   Nucleotide sequence of ORF15 encoding S-adenosylmethionine synthetase.
XX
KW   Narbonolide synthase; polyketide synthase gene; narbonolide polyketide;
KW   antibiotic; C12-hydroxyalse; picK; desosamine biosynthesis;
KW   desosaminyl transferase enzyme; ketolide; beta-glucosidase enzyme;
KW   picromycin biosynthesis; ss.
XX
OS   Streptomyces venezuelae.
XX
PN   US6117659-A.
XX
PD   12-SEP-2000.
XX
PF   27-MAY-1999;   99US-0320878.
XX
PR   28-MAY-1998;   98US-0087080.
PR   22-SEP-1998;   98US-0100880.
PR   08-FEB-1999;   99US-0119139.
PR   20-MAY-1999;   99US-0134990.
PR   30-APR-1997;   97US-0846247.
PR   06-MAY-1998;   98US-0073538.
PR   28-AUG-1998;   98US-0141908.
XX
PA   (KOSA-) KOSAN BIOSCIENCES INC.
XX
PI   Ashley G,  Betlach MC,  Betlach M,  Tang L,  McDaniel R;
XX
DR   WPI; 2000-610844/58.
XX
PT   New recombinant picK hydroxylase gene of Streptomyces venezuelae useful
PT   for converting ketolides to antibiotics and as antibiotics and
PT   intermediates in the synthesis of compounds with pharmaceutical value
PT   -
XX
PS   Disclosure; Columns 45-46; 117pp; English.
XX
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```
CC   The present sequence is used to produce the recombinant DNA compounds
CC   of the invention. The specification describes a recombinant DNA compound
CC   expressing recombinant polyketide synthase genes in host cells for the
CC   production of narbonolide, narbonolide derivatives and polyketides that
CC   are useful as antibiotics and as intermediates in the synthesis of
CC   compounds with pharmaceutical value. The DNA compounds may also encode
CC   a C12-hydroxyalse (picK), desosamine biosynthesis and desosaminyl
CC   transferase enzymes (useful for conversion of ketolides to antibiotics),
CC   and the beta-glucosidase enzyme (involved in picromycin biosynthesis).
CC   These compounds are also useful for increasing the antibiotic activity
CC   of a compound relative to the unhydroxylated compound. The recombinant
CC   host cells are useful as genetic systems that allow rapid engineering
CC   of the narbonolide polyketide synthase. These would be valuable for
CC   creating novel ketolide analogs for pharmaceutical applications.
XX
SQ   Sequence 1693 BP; 237 A; 566 C; 633 G; 257 T; 0 other;

  Query Match             16.8%;  Score 39.4;  DB 21;  Length 1693;
  Best Local Similarity   47.3%;  Pred. No. 0.0033;
  Matches   52;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy     113 ACGTACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGGTTCATCAAGA 172
           || | ||                                          |  | |  | |||
Db     848 ACCTCCGCCCGGCCGCGATCATCCGCGACCTCGACCTGCTCCGCCCGATCTACTCCCAGA 789

Qy     173 CCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 222
           ||||||| |||||||||||| ||||| ||     | ||||||||||| |||
Db     788 CCGCCGCCTACGGCCACTTCGGCCGCGAGCTGCCGGACTTCACCTGGGAG 739


RESULT 25
AAZ56005/c
ID   AAZ56005 standard; DNA; 1693 BP.
XX
AC   AAZ56005;
XX
DT   23-MAR-2000  (first entry)
XX
DE   Contig 004 from cosmid pKOS023-27 from Streptomyces venezuelae.
XX
KW   Narbonolide polyketide synthase; PKS; cosmid pKOS023-27; contig 004;
KW   ketolide; SAM synthase; S-adenosylmethionine synthase; hydroxylase;
KW   picromycin; antibiotic production; narbomycin; ds.
XX
OS   Streptomyces venezuelae.
XX
FH   Key             Location/Qualifiers
FT   CDS             complement (694..1692)
FT                   /*tag= a
FT                   /product= SAM_synthase
FT                   /note= "Partial S-adenosylmethionine synthase"
FT   CDS             complement (3..692)
FT                   /*tag= b
FT                   /product= ORF16_product
FT                   /note= "M. tuberculosis cbhK homologous partial protein"
XX
PN   WO9961599-A2.
XX
PD   02-DEC-1999.
XX
PF   27-MAY-1999;   99WO-US11814.
XX
PR   28-MAY-1998;   98US-0087080.
PR   28-AUG-1998;   98US-0141908.
PR   22-SEP-1998;   98US-0100880.
PR   08-FEB-1999;   99US-0119139.
XX
PA   (KOSA-) KOSAN BIOSCIENCES INC.
XX
PI   Ashley G,  Betlach MC,  Betlach M,  McDaniel R,  Tang L;
XX
DR   WPI; 2000-072618/06.
DR   P-PSDB; AAY67216, AAY67217.
XX
PT   New recombinant DNA encoding a domain of narbonolide polyketide
PT   synthase, for production of ketolide antibiotics -
XX
PS   Disclosure; Page 38; 98pp; English.
XX
CC   This is contig 004 from the recombinant cosmid pKOS023-27 DNA sequence
CC   (see AAZ56001) which contains a Streptomyces venezuelae DNA insert. The
CC   cosmid contains open reading frames which encode the various modules of
CC   the narbonolide polyketide synthase (PKS). The invention relates to
CC   recombinant DNA containing a coding sequence for a narbonolide PKS.
CC   Polyketides are compounds synthesised from 2-carbon units through a
CC   series of condensations and subsequent modifications. Modular PKSs are
CC   responsible for the production of many antibiotics including picromycin.
CC   The narbonolide PKS consists of a loading module, six extender modules,
CC   and two thioester domains. Four proteins make up the narbonolide PKS
CC   (PICAI, PICAII, PICAIII and PICAIV). PICAI includes the loading module
CC   and extender modules 1 and 2, PICAII includes extender modules 3 and 4,
CC   PICAIII includes extender module 5 and PICAIV includes extender module 6
CC   and a type II thioesterase domain. The second type II thioesterase
CC   domain is found on the PICB protein. The nucleotide sequences encoding
CC   all of these proteins can be isolated in recombinant form from the
CC   recombinant cosmid pKOS023-27. Narbonolide is desosaminylated in S.
CC   venezuelae to yield narbomycin, the desosaminyl transferase enzyme is
CC   required for this conversion, and the desosamine biosynthetic genes are
CC   also found in cosmid pKOS023-27. The recombinant DNA of the invention is
CC   used to express, in transformed cells, narbonolide (or its derivatives)
CC   or other ketolides (particularly hybrids), which may then be converted
CC   (e.g. by other enzymes recombinantly expressed in the same hosts) to
CC   polyketide antibiotics or their intermediates. The antibiotics are useful
CC   in human or veterinary medicine.
XX
SQ   Sequence 1693 BP; 237 A; 566 C; 633 G; 257 T; 0 other;

  Query Match             16.8%;  Score 39.4;  DB 21;  Length 1693;
  Best Local Similarity   47.3%;  Pred. No. 0.0033;
  Matches   52;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy     113 ACGTACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGGTTCATCAAGA 172
           || | ||                                          |  | |  | |||
Db     848 ACCTCCGCCCGGCCGCGATCATCCGCGACCTCGACCTGCTCCGCCCGATCTACTCCCAGA 789

Qy     173 CCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 222
           ||||||| |||||||||||| ||||| ||     | ||||||||||| |||
Db     788 CCGCCGCCTACGGCCACTTCGGCCGCGAGCTGCCGGACTTCACCTGGGAG 739


RESULT 26
ABL72111
ID   ABL72111 standard; cDNA; 297 BP.
XX
AC   ABL72111;
XX
DT   14-MAY-2002  (first entry)
XX
DE   Corn tassel-derived polynucleotide (cdps) SEQ ID NO:1485.
XX
KW   Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPs;
KW   inheritance; characteristic; growth; development; disease resistance;
KW   environmental adaptability; quality; yield; molecular marker;
KW   multigene trait; plant breeding; corn tassel; gene; ss.
XX
OS   Zea mays.
XX
PN   US2001051335-A1.
XX
PD   13-DEC-2001.
XX
PF   16-APR-1999;   99US-0294093.
XX
PR   21-APR-1998;   98US-082567P.
XX
PA   (LALG/) LALGUDI R V.
```

PA (ITOL/) ITO L Y.
PA (SHER/) SHERMAN B K.
XX
PI Lalgudi RV, Ito LY, Sherman BK;
XX
DR WPI; 2002-163647/21.
XX
PT Novel purified corn tassel-derived polynucleotide useful for
PT determining altered gene expression, to recover regulatory elements and
PT to follow inheritance of desirable characteristics through hybrid
PT breeding programs -
XX
PS Claim 1; SEQ ID 1485; 201pp; English.
XX
CC The present sequence describes a purified corn tassel-derived
CC polynucleotide sequence (cdps) comprising a nucleic acid sequence
CC selected from those given in ABL70627 to ABL76833. The cdps sequences
CC encode corn tassel-derived polypeptides (CDPs). The cdps sequences (I)
CC can be used for determining altered gene expression, to recover
CC regulatory elements and to follow inheritance of desirable
CC characteristics through hybrid breeding programs. (I) are also useful
CC in the evaluation, and alteration of desired characteristics associated
CC with growth and development, disease resistance, environmental
CC adaptability, quality and yield, and as molecular markers for studying
CC inheritance of multigene traits in a plant breeding program. (I) can be
CC used to produce a tassel-specific profile of gene transcription, a
CC transcript image, to clone regulatory elements for use in transformation
CC vectors, to express a polypeptide, to identify, isolate or extend
CC identical or related corn tassel nucleic acid sequences from DNA
CC libraries, in nucleic acid hybridisation or amplification technologies,
CC as query sequences to determine homology of known sequences, as probe
CC for use in Southern or Northern hybridisation, and to identify the
CC presence of and/or to determine the degree of similarity between two
CC (or more) nucleic acid sequences.
XX
SQ Sequence 297 BP; 58 A; 85 C; 77 G; 50 T; 27 other;

Query Match 15.9%; Score 37.4; DB 24; Length 297;
Best Local Similarity 78.6%; Pred. No. 0.0076;
Matches 44; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 161 GGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACC 216
Db 242 GCTACCTCAAGACGGCGGCCTACGGCNACTTTGGAAGGGACGACCCTGACTTCACC 297

RESULT 27
AAA81476
ID AAA81476 standard; DNA; 56485 BP.
XX
AC AAA81476;
XX
DT 04-DEC-2000 (first entry)
XX
DE N. meningitidis partial DNA sequence gnm_24 SEQ ID NO:24.
XX
KW Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic;
KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
KW Meningococcus B; MenB; ds.
XX
OS Neisseria meningitidis.
XX
PN WO200022430-A2.
XX
PD 20-APR-2000.
XX
PF 08-OCT-1999; 99WO-US23573.
XX
PR 09-OCT-1998; 98US-0103794.
PR 30-APR-1999; 99US-0132068.
XX
PA (CHIR) CHIRON CORP.
XX
PI Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;
PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
PI Rappuoli R, Pizza M;
XX
DR WPI; 2000-318079/27.
XX
PT Isolated nucleotide sequences of Neisseria meningitidis which can be
PT used in the diagnosis and treatment of N. meningitidis infection and
PT other Neisserial infections, for example, N.gonorrhoea -
XX
PS Claim 7; Page 507-524; 1760pp; English.
XX
CC The present invention describes methods of obtaining immunogenic
CC proteins from Neisseria genomic sequences. AAA81453 to AAA82414
CC represent specifically claimed Neisseria meningitidis genomic DNA
CC sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
CC Neisseria DNA sequences and their corresponding proteins; AAA81254 to
CC AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
CC isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
CC AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
CC sequences, which are all used in the exemplification of the present
CC invention. The nucleic acid sequences, protein sequences, and antibodies
CC against them, can be used in the manufacture of a composition. The
CC composition can be used as a medicament (or in the manufacture of a
CC medicament) for treating, preventing or diagnosing infection due to
CC Neisserial bacteria. For example, some of the identified proteins could
CC be components of vaccines against Meningococcus B; against all serotypes;
CC and/or against all pathogenic Neissariae. Identification of sequences
CC from the bacterium will also facilitate production of biological probes,
CC particularly organism-specific probes. Attempts to make efficacious
CC Meningococcus B vaccines have failed mainly due to antigen tolerance.
CC Multivalent vaccines have also been tried but none have successfully
CC overcome antigenic variability. The provision of further, complete
CC sequences may provide an opportunity to identify secreted or surface
CC exposed proteins that may be presumed targets for the immune system and
CC which are not antigenically variable or at least more conserved than
CC other more variable regions.
XX
SQ Sequence 56485 BP; 12504 A; 14247 C; 16158 G; 13573 T; 3 other;

Query Match 14.7%; Score 34.6; DB 21; Length 56485;
Best Local Similarity 44.5%; Pred. No. 0.67;
Matches 49; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 113 ACGTACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGGTTCATCAAGA 172
Db 54015 ACCTGCGCCCCAAAGGCATCGTCCAAATGCTCGATCTCTTGCGCCCGATTTACAGTAAAT 54074

Qy 173 CCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 222
Db 54075 CCGCCGCTTACGGACATTTCGGCCGCGAAGAACCTGAGTTCACTTGGGAG 54124

RESULT 28
AAF21612/c
ID AAF21612 standard; DNA; 349980 BP.
XX
AC AAF21612;
XX
DT 13-MAR-2001 (first entry)
XX
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:113.
XX
KW Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine;
KW diagnosis; antigen; detection; infection; gene therapy; antibacterial;
KW ds.
XX
OS Neisseria meningitidis.
XX
PN WO200066791-A1.
XX
PD 09-NOV-2000.
XX

```
PF   08-MAR-2000; 2000WO-US05928.
XX
PR   30-APR-1999;   99US-0132068.
PR   08-OCT-1999;   99WO-US23573.
PR   28-FEB-2000; 2000GB-0004695.
XX
PA   (CHIR ) CHIRON CORP.
PA   (GENO-) INST GENOMIC RES.
XX
PI   Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC, Masignani V;
PI   Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V, Rappuoli R;
PI   Frazer CM, Grandi G;
XX
DR   WPI; 2000-647603/62.
XX
PT   Neisseria meningitidis B full length genome sequence and open reading
PT   frames are used to detect, treat and prevent Neisserial infections -
XX
PS   Claim 7; Appendix A; 692pp; English.
XX
CC   The present invention describes the full length genome of
CC   Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607
CC   to AAF21613 represent fragments of the NMB genomic sequence, as the
CC   sequence was too long to go in a record on its own it was split into 8
CC   sequences which overlap each other at the beginning and end of each
CC   sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at
CC   the beginning of AAF21607, the last 49980 bp of AAF21607 are repeated at
CC   the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the
CC   Neisseria proteins given in AAB58550 to AAB58593, and AAF21589 to
CC   AAF21606 represent PCR primers which are used in the exemplification of
CC   the present invention. The NMB genome and fragments from it have
CC   antibacterial activity, and can be used in vaccines and gene therapy.
CC   Neisseria nucleic acids, proteins and/or antibodies which binds to the
CC   proteins can be used in compositions for treating or preventing infection
CC   due to Neisserial bacteria or as a diagnostic reagent for detecting the
CC   presence of Neisserial bacteria or of antibodies raised to Neisserial
CC   bacteria. Computers, computer memory, computer storage medium or computer
CC   databases can be used in a search to identify open reading frames (ORFs)
CC   or coding sequences within the NMB genome. The DNA sequences provide
CC   further opportunities to find antigenic or immunogenic proteins which are
CC   more effective in vaccines than the outer membrane proteins currently
CC   used.
XX
SQ   Sequence 349980 BP; 86473 A; 95646 C; 85908 G; 81953 T; 0 other;

  Query Match             14.7%;  Score 34.6;  DB 21;  Length 349980;
  Best Local Similarity   44.5%;  Pred. No. 1.5;
  Matches   49;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy     113 ACGTACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGGTTCATCAAGA 172
           || | ||                                          |  | ||  ||
Db   87639 ACCTGCGCCCCAAAGGCATCGTCCAAATGCTCGATCTCTTGCGCCCGATTTACAGTAAAT 87580

Qy     173 CCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 222
           ||||||| ||||| || || ||||| || ||  | || ||||| || |||
Db   87579 CCGCCGCTTACGGACATTTCGGCCGCGAAGAACCTGAGTTCACTTGGGAG 87530


RESULT 29
AAA81489/c
ID   AAA81489 standard; DNA; 837096 BP.
XX
AC   AAA81489;
XX
DT   04-DEC-2000  (first entry)
XX
DE   N. meningitidis partial DNA sequence gnm_37 SEQ ID NO:37.
XX
KW   Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic;
KW   antigen; vaccine; diagnosis; infection; antibacterial; identification;
KW   Meningococcus B; MenB; ds.
XX
OS   Neisseria meningitidis.
XX
PN   WO200022430-A2.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-US23573.
XX
PR   09-OCT-1998;   98US-0103794.
PR   30-APR-1999;   99US-0132068.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;
PI   Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
PI   Rappuoli R, Pizza M;
XX
DR   WPI; 2000-318079/27.
XX
PT   Isolated nucleotide sequences of Neisseria meningitidis which can be
PT   used in the diagnosis and treatment of N. meningitidis infection and
PT   other Neisserial infections, for example, N.gonorrhoea -
XX
PS   Claim 7; Page 629-865; 1760pp; English.
XX
CC   The present invention describes methods of obtaining immunogenic
CC   proteins from Neisseria genomic sequences. AAA81453 to AAA82414
CC   represent specifically claimed Neisseria meningitidis genomic DNA
CC   sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
CC   Neisseria DNA sequences and their corresponding proteins; AAA81254 to
CC   AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
CC   isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
CC   AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
CC   sequences, which are all used in the exemplification of the present
CC   invention. The nucleic acid sequences, protein sequences, and antibodies
CC   against them, can be used in the manufacture of a composition. The
CC   composition can be used as a medicament (or in the manufacture of a
CC   medicament) for treating, preventing or diagnosing infection due to
CC   Neisserial bacteria. For example, some of the identified proteins could
CC   be components of vaccines against Meningococcus B; against all serotypes;
CC   and/or against all pathogenic Neissariae. Identification of sequences
CC   from the bacterium will also facilitate production of biological probes,
CC   particularly organism-specific probes. Attempts to make efficacious
CC   Meningococcus B vaccines have failed mainly due to antigen tolerance.
CC   Multivalent vaccines have also been tried but none have successfully
CC   overcome antigenic variability. The provision of further, complete
CC   sequences may provide an opportunity to identify secreted or surface
CC   exposed proteins that may be presumed targets for the immune system and
CC   which are not antigenically variable or at least more conserved than
CC   other more variable regions.
XX
SQ   Sequence 837096 BP; 207534 A; 227065 C; 205215 G; 197280 T; 2 other;

  Query Match             14.7%;  Score 34.6;  DB 21;  Length 837096;
  Best Local Similarity   44.5%;  Pred. No. 2.1;
  Matches   49;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy     113 ACGTACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGGTTCATCAAGA 172
           || | ||                                          |  | ||  ||
Db 452410 ACCTGCGCCCCAAAGGCATCGTCCAAATGCTCGATCTCTTGCGCCCGATTTACAGTAAAT 452351

Qy     173 CCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 222
           ||||||| ||||| || || ||||| || ||  | || ||||| || |||
Db 452350 CCGCCGCTTACGGACATTTCGGCCGCGAAGAACCTGAGTTCACTTGGGAG 452301


RESULT 30
AAI99683
ID   AAI99683 standard; DNA; 4403765 BP.
XX
AC   AAI99683;
XX
DT   15-JAN-2002  (first entry)
XX
```

DE Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.
XX
KW Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
KW variation; epidemiology; patient treatment; epidemic monitoring; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN US6294328-B1.
XX
PD 25-SEP-2001.
XX
PF 24-JUN-1998; 98US-0103840.
XX
PR 24-JUN-1998; 98US-0103840.
XX
PA (GENO-) INST GENOMIC RES.
XX
PI Fleischmann RD, White OR, Fraser CM, Venter JC;
XX
DR WPI; 2001-647261/74.
XX
PT Evaluating strain variation of Mycobacterium tuberculosis, comprises
PT determining the nucleotide sequence of the strain at positions in the
PT genome corresponding to positions where M. tuberculosis strains CDC
PT 1551 and H37Rv differ -
XX
PS Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.
XX
CC The invention relates to evaluating strain variation within and between
CC different populations of the tuberculosis bacterial pathogen,
CC Mycobacterium tuberculosis or related Mycobacterium by determining the
CC nucleotide sequence of the first strain at positions in the complete
CC sequence of the genome that correspond to positions that differ in the
CC nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and
CC H37Rv (AAI99682). The method is useful for evaluating strain variation of
CC M. tuberculosis and has valuable application in the fields of
CC tuberculosis genetics, epidemiology, patient treatment and epidemic
CC monitoring.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
XX
SQ Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;

Query Match 14.6%; Score 34.4; DB 22; Length 4403765;
Best Local Similarity 73.3%; Pred. No. 5.1;
Matches 44; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 171 GACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTCAA 230
||||||||| ||||| ||||| ||||| ||||| ||| || | || ||| | || |
Db 1567783 GACCGCCGCCTACGGGCACTTCGGCCGCACCGACGTCGAATTACCGTGGGAGCAGCTCGA 1567842

RESULT 31
AAI99682
ID AAI99682 standard; DNA; 4411529 BP.
XX
AC AAI99682;
XX
DT 15-JAN-2002 (first entry)
XX
DE Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.
XX
KW Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
KW variation; epidemiology; patient treatment; epidemic monitoring; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN US6294328-B1.
XX
PD 25-SEP-2001.
XX
PF 24-JUN-1998; 98US-0103840.
XX
PR 24-JUN-1998; 98US-0103840.
XX
PA (GENO-) INST GENOMIC RES.
XX
PI Fleischmann RD, White OR, Fraser CM, Venter JC;
XX
DR WPI; 2001-647261/74.
XX
PT Evaluating strain variation of Mycobacterium tuberculosis, comprises
PT determining the nucleotide sequence of the strain at positions in the
PT genome corresponding to positions where M. tuberculosis strains CDC
PT 1551 and H37Rv differ -
XX
PS Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.
XX
CC The invention relates to evaluating strain variation within and between
CC different populations of the tuberculosis bacterial pathogen,
CC Mycobacterium tuberculosis or related Mycobacterium by determining the
CC nucleotide sequence of the first strain at positions in the complete
CC sequence of the genome that correspond to positions that differ in the
CC nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and
CC H37Rv (AAI99682). The method is useful for evaluating strain variation of
CC M. tuberculosis and has valuable application in the fields of
CC tuberculosis genetics, epidemiology, patient treatment and epidemic
CC monitoring.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
XX
SQ Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;

Query Match 14.6%; Score 34.4; DB 22; Length 4411529;
Best Local Similarity 73.3%; Pred. No. 5.1;
Matches 44; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 171 GACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTCAA 230
||||||||| ||||| ||||| ||||| ||||| ||| || | || ||| | || |
Db 1567944 GACCGCCGCCTACGGGCACTTCGGCCGCACCGACGTCGAATTACCGTGGGAGCAGCTCGA 1568003

RESULT 32
ABL09034/c
ID ABL09034 standard; cDNA; 17512 BP.
XX
AC ABL09034;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21584.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB64931.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more

```
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Claim 1; SEQ ID NO 21584; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 17512 BP; 5092 A; 3575 C; 3816 G; 5029 T; 0 other;

  Query Match             14.0%;  Score 33;  DB 23;  Length 17512;
  Best Local Similarity   41.6%;  Pred. No. 1.4;
  Matches   69;  Conservative    0;  Mismatches   97;  Indels    0;  Gaps    0;

Qy      61 TGATCCATTGTTCGTTGTGTTATTAATGTTGTATAATTGAGCAGGACACAACACGTACGT 120
           ||||  ||  ||  |  | ||   |  | || |    |||||| || | | |||| || |
Db    2465 TGATGTATATTTATTCCTTTTCGCAGGGCTGAACTTCTGAGCATGAGAGATCACGGACAT 2406

Qy     121 TNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGGTTCATCAAGACCGCCGCA 180
                                                   ||| ||   |||| |   | |
Db    2405 CATCCCATGGGACCCGTCGACTACTTCAGCATTAAGATCAGCTTTGGCAAGGGCTGGGGA 2346

Qy     181 TACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGG 226
             || | ||    | |  ||   |   | || | |||||  | |||
Db    2345 CGCGACTACAAAAGACAGGATATCATGGGCTGCCCCTGCTGGCTGG 2300


RESULT 33
AAH99804/c
ID   AAH99804 standard; cDNA; 1844 BP.
XX
AC   AAH99804;
XX
DT   16-OCT-2001  (first entry)
XX
DE   Human protein encoding cDNA sequence SEQ ID NO:639.
XX
KW   Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW   antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW   antibacterial; endocrine; cardiant; central nervous system; virucide;
KW   anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
KW   antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
KW   dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
KW   neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW   immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW   antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW   cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW   genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW   thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW   allergic rhinitis; diabetes; multiple sclerosis; depression;
KW   Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW   neurological disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200153455-A2.
XX
PD   26-JUL-2001.
XX
PF   22-DEC-2000; 2000WO-US35017.
XX
PR   23-DEC-1999;   99US-0471275.
PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-457603/49.
DR   P-PSDB; AAM25863.
XX
PT   Isolated human polynucleotides encoding polypeptides, useful for the
PT   treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
XX
PS   Claim 1; Page 659; 1217pp; English.
XX
CC   AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC   AAM25963. The proteins can have activities based on the tissues and
CC   cells they are expressed in, such as: antiinflammatory; antirheumatic;
CC   antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
CC   central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC   cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;
CC   antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
CC   antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC   antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC   encoding them can be used in gene therapy, antisense therapy and vaccine
CC   production, The proteins and polynucleotides are useful for screening for
CC   agonists or antagonists of a protein and for the treatment and diagnosis
CC   of disorders associated with the activity of a protein e.g. inflammation,
CC   rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC   neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC   infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC   anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC   osteoporosis, severe combined immunodeficiency, eczema, allergic
CC   rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC   Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC   neurological disorders.
XX
SQ   Sequence 1844 BP; 444 A; 484 C; 535 G; 380 T; 1 other;

  Query Match             13.3%;  Score 31.2;  DB 22;  Length 1844;
  Best Local Similarity   41.0%;  Pred. No. 2.3;
  Matches   66;  Conservative    0;  Mismatches   95;  Indels    0;  Gaps    0;

Qy      25 AGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATT 84
           ||  ||| | |    | ||| ||  |||   |  || |   || || |   | | || ||
Db    1635 AGCGCGATGTTTTAAAGGCTCATCCATGCTGGAGCCCGTGTCAGTGCTTCGTTTCTTTTT 1576

Qy      85 AATGTTGTATAATTGAGCAGGACACAACACGTACGTTNNNNNNNNNNNNNNNNNNNNNN 144
           |  | |  | |||||   | |      |||| ||| |
Db    1575 ATGGCTTAAAAATTGTCTATGGTGGGCCACGCACGGTGGCTCACGCCTGTAATCCCAACA 1516

Qy     145 NNNNNNNNNNNNNNCAGGTTCATCAAGACCGCCGCATACGG 185
                     ||||   |||| ||   | | | | ||
Db    1515 CTGGGAGGCCGAGGCAGGCGGATCATGAGGTCAGGAGATGG 1475


RESULT 34
AAS59515/c
ID   AAS59515 standard; DNA; 66788 BP.
XX
AC   AAS59515;
XX
DT   13-FEB-2002  (first entry)
XX
DE   Propionibacterium acnes immunogenic protein encoding DNA #10.
XX
KW   SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW   uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW   inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW   dermatological; osteopathic; neuroprotectant; ds.
XX
OS   Propionibacterium acnes.
XX
PN   WO200181581-A2.
XX
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PD   01-NOV-2001.
XX
PF   20-APR-2001; 2001WO-US12865.
XX
PR   21-APR-2000; 2000US-199047P.
PR   02-JUN-2000; 2000US-208841P.
PR   07-JUL-2000; 2000US-216747P.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Skeiky YAW,  Persing DH,  Mitcham JL,  Wang SS,  Bhatia A;
PI   L'maisonneuve J,  Zhang Y,  Jen S,  Carter D;
XX
DR   WPI; 2001-616774/71.
XX
PT   Propionibacterium acnes polypeptides and nucleic acids useful for
PT   vaccinating against and diagnosing infections, especially useful for
PT   treating acne vulgaris -
XX
PS   Claim 1; SEQ ID No 10; 1069pp; English.
XX
CC   Sequences AAS59506-AAS59804 represent DNA molecules encoding
CC   Propionibacterium acnes immunogenic polypeptides. The proteins and their
CC   associated DNA sequences are used in the treatment, prevention and
CC   diagnosis of medical conditions caused by P. acnes. The disorders include
CC   SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and
CC   osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved
CC   in infections of bone, joints and the central nervous system, however it
CC   is particularly involved in the inflammatory lesions associated with acne
CC   vulgaris. A method for detecting the presence or absence of P. acnes in a
CC   patient comprises contacting a sample with a binding agent that binds to
CC   the proteins of the invention and determining the amount of bound protein
CC   in the sample. The polypeptides may be used as antigens in the production
CC   of antibodies specific for P. acnes proteins. These antibodies can be
CC   used to downregulate expression and activity of P. acnes polypeptides and
CC   therefore treat P. acnes infections. The antibodies may also be used as
CC   diagnostic agents for determining P. acnes presence, for example, by
CC   enzyme linked immunosorbent assay (ELISA). This sequence encodes the
CC   polypeptides shown in AAU41313-42019 and AAU67473.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 66788 BP; 13534 A; 21369 C; 19347 G; 12530 T; 8 other;

  Query Match             13.1%;  Score 30.8;  DB 23;  Length 66788;
  Best Local Similarity   41.7%;  Pred. No. 15;
  Matches   53;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy     105 GACACAACACGTACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGGTT 164
           ||  |  |  | | |||                                          |  | |
Db   26120 GAAGCGTCCGGCAGGTTCGTTCATTTTTGCTGGCCCGTCGGGTGTTGGTAAGACCGAGCT 26061

Qy     165 CATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGT 224
           || |||| |   | | |   || |||||||   || ||||||  | |||||  |||  |
Db   26060 CACCAAGGCGCTCACCGAGTTCCTCTTTGGCGACGAGGACGCCCTCATCACCCTCGACAT 26001

Qy     225 GGTCAAG 231
           |  | ||
Db   26000 GAGCGAG 25994


RESULT 35
AAS51580/c
ID   AAS51580 standard; DNA; 606 BP.
XX
AC   AAS51580;
XX
DT   13-FEB-2002  (first entry)
XX
DE   Pseudomonas aeruginosa DNA for cellular proliferation protein #165.
XX
KW   Antisense; ds; prokaryotic cellular proliferation gene;
KW   antibiotic; antibacterial; drug design.
XX
OS   Pseudomonas aeruginosa.
XX
PN   WO200170955-A2.
XX
PD   27-SEP-2001.
XX
PF   21-MAR-2001; 2001WO-US09180.
XX
PR   21-MAR-2000; 2000US-191078P.
PR   23-MAY-2000; 2000US-206848P.
PR   26-MAY-2000; 2000US-207727P.
PR   23-OCT-2000; 2000US-242578P.
PR   27-NOV-2000; 2000US-253625P.
PR   22-DEC-2000; 2000US-257931P.
PR   16-FEB-2001; 2001US-269308P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Haselbeck R,  Ohlsen KL,  Zyskind JW,  Wall D,  Trawick JD,  Carr GJ;
PI   Yamamoto RT,  Xu HH;
XX
DR   WPI; 2001-611495/70.
DR   P-PSDB; AAU33721.
XX
PT   New polynucleotides for the identification and development of
PT   antibiotics, comprise sequences of antisense nucleic acids -
XX
PS   Claim 27; Seq ID No 4162; 511pp; English.
XX
CC   The invention relates to antisense inhibitors of genes essential to
CC   prokaryotic cellular proliferation, their use in identifying the
CC   genes, their use in the discovery of novel antibiotics, the essential
CC   genes themselves and the encoded proteins. The prokaryotes used are
CC   Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC   pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC   invention is also useful for the identification of potential new targets
CC   for antibiotic development. The antisense nucleic acids can also be used
CC   to identify proteins used in proliferation, to express these proteins,
CC   and to obtain antibodies capable of binding to the expressed proteins.
CC   The proteins can be used to screen compounds in rational drug discovery
CC   programmes. The antisense nucleic acid sequence is also useful to screen
CC   for homologous nucleic acids which are required for cell proliferation in
CC   a wide variety of organisms. The present sequence encodes an
CC   essential prokaryotic cellular proliferation protein.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic
CC   format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 606 BP; 121 A; 212 C; 185 G; 88 T; 0 other;

  Query Match             13.0%;  Score 30.6;  DB 23;  Length 606;
  Best Local Similarity   68.9%;  Pred. No. 2.3;
  Matches   42;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy     174 CGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTCAAGCC 233
           ||||||||||  ||  |||| |||  | |  || || | || || |||   ||| |||| |
Db     106 CGCCGCATACCGCGGCTTTCGCCTGGCCCGCGGCGGCATCGCCAGCGGCATGGGCAAGGC 47

Qy     234 C 234
           |
Db      46 C 46


RESULT 36
AAF12426
ID   AAF12426 standard; cDNA; 657 BP.
XX
AC   AAF12426;
XX
DT   13-MAR-2001  (first entry)
```

```
XX
DE   Aspergillus oryzae EST SEQ ID NO:4949.
XX
KW   Multiple gene expression; filamentous fungal cell; EST;
KW   expressed sequence tag; Fusarium venenatum; Aspergillus niger;
KW   Aspergillus oryzae; Trichoderma reesei; identification; recombination;
KW   culture condition; environmental stress; spore morphogenesis;
KW   metabolic pathway engineering; catabolic pathway engineering; ss.
XX
OS   Aspergillus oryzae.
XX
PN   WO200056762-A2.
XX
PD   28-SEP-2000.
XX
PF   22-MAR-2000; 2000WO-US07781.
XX
PR   22-MAR-1999;   99US-0273623.
XX
PA   (NOVO ) NOVO NORDISK BIOTECH INC.
PA   (NOVO ) NOVO NORDISK AS.
XX
PI   Berka RM,  Rey MW,  Shuster JR,  Kauppinen S,  Clausen IG,  Olsen PB;
XX
DR   WPI; 2000-594572/56.
XX
PT   Monitoring differential expression of genes in filamentous fungal cells
PT   uses fluorescence-labeled nucleic acids isolated from the cells and a
PT   substrate of expressed sequence tags -
XX
PS   Claim 88; Page 2084; 3161pp; English.
XX
CC   The present invention describes a method for monitoring differential
CC   expression of genes in a first filamentous fungal (FF) cell relative to
CC   expression of the same genes in one or more second filamentous fungal
CC   cells. The method uses fluorescence-labeled nucleic acids isolated from
CC   the FF cells and a substrate of expressed sequence tags (EST). The ESTs
CC   are used in the methods for monitoring differential expression of genes
CC   in a first filamentous fungal (FF) cell relative to expression of the
CC   same genes in one or more second filamentous fungal cells. Monitoring
CC   the global expression of genes from FF cells allows the production
CC   potential of the microorganisms to be improved. New genes may be
CC   discovered, possible functions of unknown open reading frames can be
CC   identified and gene copy number variation and stability can be
CC   monitored. The expression of genes can be used to study how FF cells
CC   adapt to changes in culture conditions, environmental stress, spore
CC   morphogenesis, recombination, metabolic or catabolic pathway
CC   engineering. Using ESTs provides several advantages over genomic or
CC   random cDNA clones including elimination of redundancy as one spot on an
CC   array equals one gene or open reading frame, and organisation of the
CC   microarrays based on function of the gene products to facilitate
CC   analysis of the results. AAF07478 to AAF11247 represents ESTs from
CC   Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
CC   niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
CC   AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
CC   all specifically claimed in the present invention.
XX
SQ   Sequence 657 BP; 155 A; 175 C; 134 G; 193 T; 0 other;

  Query Match            13.0%;  Score 30.6;  DB 21;  Length 657;
  Best Local Similarity   41.8%;  Pred. No. 2.3;
  Matches   51;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy     113 ACGTACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGGTTCATCAAGA 172
           || |   |                                          || |  |||  |
Db     174 ACCTGATTCCTGGCCTCAGCTTGCGTGCCCCGGAAGAAGACGAGATCATGGGCATTGACG 233

Qy     173 CCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTCAAGC 232
            ||||| |   ||| | ||||    |||| ||| |||  | ||| |||| ||| |||
Db     234 ACGCCGAAATTGGCGAGTTTGCTTATGACTACGTCGAGATTACCCGCGACGTGATCAGTG 293

Qy     233 CC 234
           ||
Db     294 CC 295


RESULT 37
ABL29661
ID   ABL29661 standard; DNA; 2247 BP.
XX
AC   ABL29661;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 40456.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Claim 1; SEQ ID NO 40456; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2247 BP; 733 A; 488 C; 463 G; 563 T; 0 other;

  Query Match            13.0%;  Score 30.6;  DB 23;  Length 2247;
  Best Local Similarity   41.8%;  Pred. No. 4;
  Matches   51;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy      95 AATTGAGCAGGACACAACACGTACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 154
           |||||| |   |  | ||| ||
Db     924 AATTGACCGATAAGCGACAGGTTTCAAAAGAGCGCGGCGAACAATTGGCCATCGAGTATG 983

Qy     155 NNNNCAGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCA 214
               || ||||||  ||||| |||| | | |  | ||  |   || || |||  | |||
Db     984 GCATCAAGTTCATGGAGACCTCCGCGAAGGCCAGCATTAACGTGGAAGAAGCCTTCCTCA 1043

Qy     215 CC 216
           ||
Db    1044 CC 1045


RESULT 38
AAF08527
ID   AAF08527 standard; cDNA; 566 BP.
```

```
XX
AC   AAF08527;
XX
DT   13-MAR-2001  (first entry)
XX
DE   Fusarium venenatum EST SEQ ID NO:1050.
XX
KW   Multiple gene expression; filamentous fungal cell; EST;
KW   expressed sequence tag; Fusarium venenatum; Aspergillus niger;
KW   Aspergillus oryzae; Trichoderma reesei; identification; recombination;
KW   culture condition; environmental stress; spore morphogenesis;
KW   metabolic pathway engineering; catabolic pathway engineering; ss.
XX
OS   Fusarium venenatum.
XX
PN   WO200056762-A2.
XX
PD   28-SEP-2000.
XX
PF   22-MAR-2000; 2000WO-US07781.
XX
PR   22-MAR-1999;   99US-0273623.
XX
PA   (NOVO ) NOVO NORDISK BIOTECH INC.
PA   (NOVO ) NOVO NORDISK AS.
XX
PI   Berka RM,  Rey MW,  Shuster JR,  Kauppinen S,  Clausen IG,  Olsen PB;
XX
DR   WPI; 2000-594572/56.
XX
PT   Monitoring differential expression of genes in filamentous fungal cells
PT   uses fluorescence-labeled nucleic acids isolated from the cells and a
PT   substrate of expressed sequence tags -
XX
PS   Claim 86; Page 782-783; 3161pp; English.
XX
CC   The present invention describes a method for monitoring differential
CC   expression of genes in a first filamentous fungal (FF) cell relative to
CC   expression of the same genes in one or more second filamentous fungal
CC   cells. The method uses fluorescence-labeled nucleic acids isolated from
CC   the FF cells and a substrate of expressed sequence tags (EST). The ESTs
CC   are used in the methods for monitoring differential expression of genes
CC   in a first filamentous fungal (FF) cell relative to expression of the
CC   same genes in one or more second filamentous fungal cells. Monitoring
CC   the global expression of genes from FF cells allows the production
CC   potential of the microorganisms to be improved. New genes may be
CC   discovered, possible functions of unknown open reading frames can be
CC   identified and gene copy number variation and stability can be
CC   monitored. The expression of genes can be used to study how FF cells
CC   adapt to changes in culture conditions, environmental stress, spore
CC   morphogenesis, recombination, metabolic or catabolic pathway
CC   engineering. Using ESTs provides several advantages over genomic or
CC   random cDNA clones including elimination of redundancy as one spot on an
CC   array equals one gene or open reading frame, and organisation of the
CC   microarrays based on function of the gene products to facilitate
CC   analysis of the results. AAF07478 to AAF11247 represents ESTs from
CC   Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
CC   niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
CC   AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
CC   all specifically claimed in the present invention.
XX
SQ   Sequence 566 BP; 127 A; 164 C; 129 G; 122 T; 24 other;

  Query Match             12.9%;  Score 30.2;  DB 21;  Length 566;
  Best Local Similarity   40.6%;  Pred. No. 3;
  Matches   69;  Conservative    0;  Mismatches  101;  Indels    0;  Gaps    0;

Qy      64 TCCATTGTTCGTTGTGTTATTAATGTTGTATAATTGAGCAGGACACAACACGTACGTTNN 123
           || |||| |  |  |    | ||  |    || | |  |    |      | | ||
Db      25 TCAATTGCTTCTCCTCGATTCAAAATGAAGTACTCGCTCGCCCCCTTNATCCTCCGCCGG 84

Qy     124 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGGTTCATCAAGACCGCCGCATAC 183
                       |                    | ||| | | || || ||||  |||

Db      85 CCGTGGCTCGCCCGNTTTTTCAAGCCCGCCGCTACCTGGTACGTNAACACTGCCGGGTAC 144

Qy     184 GGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTCAAGCC 233
           ||||  | ||||   |  ||| |||  ||  |   |||| |  | || |
Db     145 CGCCAGATGGGCCTCAAATACGACGATCTCCTCGAGGAGGAGAACGAGAC 194


RESULT 39
AAV64373
ID   AAV64373 standard; cDNA; 1519 BP.
XX
AC   AAV64373;
XX
DT   15-FEB-1999  (first entry)
XX
DE   GABA-gated chloride channel TBW-a3 cDNA.
XX
KW   TBW-a3; GABA-gated chloride channel; tobacco budworm; insecticide;
KW   ss.
XX
OS   Heliothis virescens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1446
FT                   /*tag=  a
FT   sig_peptide     1..66
FT                   /*tag=  b
FT   sig_peptide     67..1443
FT                   /*tag=  c
XX
PN   WO9849185-A1.
XX
PD   05-NOV-1998.
XX
PF   27-APR-1998;   98WO-US08563.
XX
PR   02-JAN-1998;   98US-0002361.
PR   28-APR-1997;   97US-0044976.
XX
PA   (FMCC ) FMC CORP.
XX
PI   Halling BP,  Yuhas DA;
XX
DR   WPI; 1999-009411/01.
DR   P-PSDB; AAW81635-36.
XX
PT   New isolated Lepidoptera GABA-gated chloride channels - comprise 3
PT   isoforms isolated from the tobacco budworm Heliothis virescens, used
PT   for characterising bioactive agents, e.g. insecticides
XX
PS   Claim 1d; Fig 2; 55pp; English.
XX
CC   This cDNA sequence encompasses the open reading frame encoding
CC   GABA-gated chloride channel TBW-a3 (see AAW81635-36) of tobacco
CC   budworm (Heliothis virescens).  TBW-a3, TBW-a2 (see AAW81633-34)
CC   and TBW-a1 (see AAW81637) proteins are 3 receptor isoforms that show
CC   sequence homology to each other and to other insect GABA-gated
CC   chloride channels.  TBW-2a cDNA was obtained from H. virescens 4th
CC   instar larva RNA by PCR and RACE amplifications.  The invention
CC   provides expression vectors in which a nucleic acid encoding a
CC   GABA-gated chloride channel is driven by an inducible promoter, and
CC   a claimed process for producing a GABA-gated chloride channel by
CC   transformed cells.   The GABA-gated channels or cells expressing
CC   them can be used for characterising a bioactive agent (claimed),
CC   e.g. for use as an insecticide.  Probes and primers that identify
CC   or amplify GABA-gated chloride channel nucleic acids of the
CC   invention are also claimed.
XX
SQ   Sequence 1519 BP; 421 A; 362 C; 347 G; 388 T; 1 other;

  Query Match             12.7%;  Score 29.8;  DB 20;  Length 1519;
  Best Local Similarity   40.5%;  Pred. No. 6.3;
  Matches   64;  Conservative    0;  Mismatches   94;  Indels    0;  Gaps    0;
```

```
Qy      2 TTTTCCGTCTAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCT 61
          |||| | ||   |     ||||| ||||  || |   ||| |  | |||    |||   |
Db    253 TTTTACTTCAGACAATTTTGGACTGATCCTCGATTAGCATACAAAAAAAGAACCGGAGTT 312

Qy     62 GATCCATTGTTCGTTGTGTTATTAATGTTGTATAATTGAGCAGGACACAACACGTACGTT 121
          ||  | || |  || | | |  | |  |  | ||   | ' | || | |||||| | ||
Db    313 GAAACTTTATCTGTGGGCTCAGAATTCATAAAGAACATATGGGTACCCGACACGTTCTTT 372

Qy    122 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNC 159
                                              |
Db    373 GTAAATGAAAAGCAATCTTATTTCCATATAGCAACAAC 410
```

RESULT 40
ABL09035
ID ABL09035 standard; cDNA; 3550 BP.
XX
AC ABL09035;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21587.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB64932.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 21587; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 3550 BP; 1070 A; 899 C; 798 G; 783 T; 0 other;

```
  Query Match           12.6%;  Score 29.6;  DB 23;  Length 3550;
  Best Local Similarity  40.7%;  Pred. No. 11;
  Matches   59;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy     82 ATTAATGTTGTATAATTGAGCAGGACACAACACGTACGTTNNNNNNNNNNNNNNNNNNNNN 141
          | ||  | || |    ||||| || | | |||| || |
Db   2107 AATAGGGCTGAACTTCTGAGCATGAGAGATCACGGACATCATCCCATGGGACCCGTCGAC 2166
```

```
Qy    142 NNNNNNNNNNNNNNNNNCAGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGAC 201
                            ||| ||   ||||  |   | |  || | ||    | |  ||
Db   2167 TACTTCAGCATTAAGATCAGCTTTGGCAAGGGCTGGGGACGCGACTACAAAAGACAGGAT 2226

Qy    202 GACGCCGACTTCACCTGCGAGGTGG 226
            |   | || | |||||  | |||
Db   2227 ATCATGGGCTGCCCCTGCTGGCTGG 2251
```

RESULT 41
AAT86246/c
ID AAT86246 standard; cDNA to mRNA; 1683 BP.
XX
AC AAT86246;
XX
DT 07-JAN-1998 (first entry)
XX
DE cDNA encoding mugwort pollen co-factor-independent phosphoglycerate
DE mutase isoform Art17.
XX
KW Cofactor-independent phosphoglycerate mutase; PGM-i; E.C. 5.4.21;
KW Mugwort; pollen; allergy; plant allergen; panallergen; B cell;
KW T cell; epitope; immunotherapy; detection; diagnosis; hay fever;
KW conserved; ds.
XX
OS Artemisia vulgaris.
XX
FH Key   Location/Qualifiers
FT CDS   1..1683
FT   /*tag= a
XX
PN WO9705258-A2.
XX
PD 13-FEB-1997.
XX
PF 02-AUG-1996;   96WO-AT00141.
XX
PR 02-AUG-1995;   95AT-0001320.
XX
PA (BIOM-) BIOMAY PRODN & HANDELS GMBH.
XX
PI Breitenbach M, Ebner C, Engel E, Ferreira F, Jilek A;
PI Kraft D, Richter K, Rheinberger H;
XX
DR WPI; 1997-145695/13.
DR P-PSDB; AAW28505.
XX
PT New recombinant DNA encoding plant phospho:glycerate mutase or its
PT antigenic epitope(s) - useful for diagnosis or treatment of
PT allergies to pollen and plant-derived foods
XX
PS Claim 1; Fig 10b; 160pp; German.
XX
CC AAT86246 encodes mugwort pollen co-factor-independent phosphoglycerate
CC mutase (PGM-i) isoform Art17. PGM-i is a highly conserved plant allergen
CC (panallergen) which can cause cross-reactivity in patients allergic to
CC pollen and plant-derived foods. PGM-i and it's B cell and T cell
CC epitopes can be used for the in vitro detection of allergy against
CC PGM-i, by measuring serum IgE or a cellular reaction. They can also be
CC used in immunotherapy and will not cause an autoimmune response because
CC PGM-i is significantly different from the human enzyme, which is
CC co-factor dependent.
XX
SQ Sequence 1683 BP; 466 A; 304 C; 456 G; 457 T; 0 other;

```
  Query Match           12.5%;  Score 29.4;  DB 18;  Length 1683;
  Best Local Similarity  40.9%;  Pred. No. 9.1;
  Matches   54;  Conservative    0;  Mismatches   78;  Indels    0;  Gaps    0;

Qy     98 TGAGCAGGACACAACACGTACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 157
          ||| | | |  || ||| ||  ||
Db   1421 TGATCCGCAGTCACCACATATATTCCACCTACTTCCTTTATTGCATCAAGGATCATCTTA 1362
```

```
Qy     158 NCAGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCT 217
           |||  ||||||  | |   |||| |  | ||| | |||   | | | |||   |  ||
Db    1361 ACAGCATCATCAGCAGCCTTGCATGCCACAACTGTTGCCTCAATGTCACCGGTATGCCCA 1302

Qy     218 GCGAGGTGGTCA 229
           | | ||   ||
Db    1301 ACCATGTCACCA 1290


RESULT 42
AAZ49567
ID   AAZ49567 standard; cDNA; 1557 BP.
XX
AC   AAZ49567;
XX
DT   07-APR-2000  (first entry)
XX
DE   Maize MLO9 protein encoding cDNA.
XX
KW   MLO9 protein; ZmMLO9; mutation; recessive allele; disease resistance;
KW   pathogen; anti-infective; antipathogenic; antiviral; antifungal;
KW   antihelminthic; anti-arthropod; maize; ss.
XX
OS   Zea mays.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1410
FT                   /*tag=  a
FT                   /product= "MLO9 protein"
XX
PN   WO200001722-A1.
XX
PD   13-JAN-2000.
XX
PF   07-JUL-1999;   99WO-US15255.
XX
PR   07-JUL-1998;   98US-0091875.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Briggs SP,  Simmons CR;
XX
DR   WPI; 2000-137196/12.
DR   P-PSDB; AAY44608.
XX
PT   Creating or enhancing disease resistance in plants by modulating plant
PT   resistance genes expression  -
XX
PS   Claim 1c; Page 80; 88pp; English.
XX
CC   The present cDNA sequence encodes maize MLO9 (ZmMLO9) protein. Mlo9 gene
CC   is a mutation-induced recessive allele, that confers resistance to
CC   plant pathogens. Expression of native Mlo genes in plants can be altered
CC   by transforming them with a DNA construct comprising the mutated Mlo
CC   gene. Decreasing the expression or activity of native MLO protein leads
CC   to enhanced resistance of plants against pathogens such as fungi, virus,
CC   nematodes and insects. Mlo gene can be used to isolate related sequences
CC   from other plants and as molecular markers used in breeding programs
CC   aimed at improving disease resistance. MLO protein has anti-infective,
CC   antipathogenic, antiviral, antifungal, antihelminthic and anti-arthropod
CC   activity.
XX
SQ   Sequence 1557 BP; 383 A; 381 C; 424 G; 369 T; 0 other;

  Query Match             12.4%;  Score 29.2;  DB 21;  Length 1557;
  Best Local Similarity   40.9%;  Pred. No. 10;
  Matches   52;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy      71 TTCGTTGTGTTATTAATGTTGTATAATTGAGCAGGACACAACACGTACGTTNNNNNNNNN 130
           ||||||||    || ||||| | ||||  ||  |||  ||||  |||| ||
Db     508 TTCGTTGTTGCTTTTATGTTATTTAATGTAGACGGATCCAACCTGTACTTTTGGATAGCA 567

Qy     131 NNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGGTTCATCAAGACCGCCGCATACGGCCACT 190
                                          ||| ||      | ||     |  || |||
Db     568 ATTCTTCCTGTAACTCTTGTTCTTCTGGTGGGTGCAAAGCTGCAGCATGTGATTGCGACT 627

Qy     191 TTGGCCG 197
           |  | |
Db     628 CTAACAG 634


RESULT 43
AAA48576
ID   AAA48576 standard; cDNA; 2604 BP.
XX
AC   AAA48576;
XX
DT   19-SEP-2000  (first entry)
XX
DE   cDNA encoding wheat protein phosphatase 2A regulatory subunit A.
XX
KW   Wheat; protein phosphatase 2A; protein phosphorylation modulation;
KW   transgenic plant; gene therapy; ss.
XX
OS   Triticum aestivum.
XX
FH   Key             Location/Qualifiers
FT   CDS             101..2028
FT                   /*tag=  a
FT                   /product= "protein phosphatase 2A regulatory
FT                   subunit A"
FT                   /note= "contains an intron"
FT   exon            101..1537
FT                   /*tag=  b
FT                   /number= 1
FT   intron          1538..1794
FT                   /*tag=  c
FT                   /number= 1
FT   exon            1795..2028
FT                   /*tag=  d
FT                   /number= 2
XX
PN   WO200036121-A2.
XX
PD   22-JUN-2000.
XX
PF   15-DEC-1999;   99WO-US29823.
XX
PR   16-DEC-1998;   98US-0112541.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Famodu OO,  Miao G,  Sakai H,  Lee J,  Rafalski JA,  Klein TM;
XX
DR   WPI; 2000-431599/37.
DR   P-PSDB; AAY99821.
XX
PT   Polynucleotides encoding plant protein phosphatase useful for
PT   modulating reversible protein phosphorylation in plants -
XX
PS   Claim 4; Page 59; 73pp; English.
XX
CC   The present sequence encodes wheat protein phosphatase 2A regulatory
CC   subunit A. The sequence was identified in clone wr1.pk0030.b10:fis of a
CC   cDNA library made from the root of a seven-day-old wheat seedling.
CC   BLAST analysis showed that the present sequence encodes protein
CC   phosphatase 2A regulatory subunit A. The sequence may be used
CC   for the recombinant production of the protein in vivo, e.g. via a gene
CC   therapy protocol, or in vitro, e.g. in fermentation culture. The protein
CC   may then be used to modulate the process of reversible protein
CC   phosphorylation in plants. It may be used directly to supplement a
CC   plant's own production of the enzyme or to rectify mutations that result
CC   in the expression of inactive protein. The protein may also be used to
CC   test for modulators of protein phosphorylation which may be used to
CC   alter the activity of the enzyme.
XX
```

```
SQ   Sequence 2604 BP; 779 A; 515 C; 579 G; 731 T; 0 other;

  Query Match           12.4%;  Score 29.2;  DB 21;  Length 2604;
  Best Local Similarity   75.8%;  Pred. No. 13;
  Matches   50;  Conservative    0;  Mismatches   13;  Indels    3;  Gaps    1;

Qy      38 CCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTAATGTTGTATAAT 97
           |||||||||||  |   ||  ||| ||| | |   |  ||||||||||||||||||||
Db    2330 CCATGCTGATAATGGATGGGCTCTGTTCCCCTTT---TGTTGTTATTAATGTTGTATAAT 2386

Qy      98 TGAGCA 103
           ||||||
Db    2387 TGAGCA 2392


RESULT 44
ABL04431/c
ID   ABL04431 standard; cDNA; 1086 BP.
XX
AC   ABL04431;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 7775.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ss.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   P-PSDB; ABB60328.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Claim 1; SEQ ID NO 7775; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1086 BP; 295 A; 267 C; 273 G; 251 T; 0 other;

  Query Match           12.3%;  Score 29;  DB 23;  Length 1086;
  Best Local Similarity   40.0%;  Pred. No. 10;
  Matches   68;  Conservative    0;  Mismatches  102;  Indels    0;  Gaps    0;

Qy      36 GCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTAATGTTGTATA 95
           ||||||     ||| |||| |||||   ||| | |  |||| |       | ||  || |
Db     943 GCCCATATCCGTAACTGGAGGGTCCCCCTCCGTAGGACGTTATTCCGGCTAGGTAATAAA 884

Qy      96 ATTGAGCAGGACACAACACGTACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 155
           ||||| ||| || |    |   ||
Db     883 ATTGATCAGCACCCCTGCCCACCGAAGCCATCAGCGGGCTACCGGAATCTCCCAGTCCGG 824

Qy     156 NNNCAGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACG 205
               | |   ||||    ||   |       |    || || |  |||||
Db     823 TGTCGGTGCCATCCCATCCCATGGCACATATCTGGATGTCCTTATCGACG 774


RESULT 45
AAH66738
ID   AAH66738 standard; DNA; 1221 BP.
XX
AC   AAH66738;
XX
DT   26-SEP-2001  (first entry)
XX
DE   C glutamicum coding sequence fragment SEQ ID NO: 1773.
XX
KW   Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW   organic acid synthesis; ds.
XX
OS   Corynebacterium glutamicum.
XX
PN   EP1108790-A2.
XX
PD   20-JUN-2001.
XX
PF   18-DEC-2000; 2000EP-0127688.
XX
PR   16-DEC-1999;   99JP-0377484.
PR   07-APR-2000; 2000JP-0159162.
PR   03-AUG-2000; 2000JP-0280988.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Nakagawa S,  Mizoguchi H,  Ando S,  Hayashi M,  Ochiai K,  Yokoi H;
PI   Tateishi N,  Senoh A,  Ikeda M,  Ozaki A;
XX
DR   WPI; 2001-376931/40.
DR   P-PSDB; AAG91519.
XX
PT   Novel polynucleotides derived from Coryneform bacteria, for identifying
PT   mutation point of a gene, measuring expression of a gene, analysing
PT   expression profile or pattern of a gene and identifying homologous gene
PT   -
XX
PS   Claim 8; SEQ ID NO: 1773; 246pp + Sequence Listing; English.
XX
CC   The present invention provides a number of nucleotide and protein
CC   sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC   are useful for identifying the mutation point of a gene derived from a
CC   mutant of coryneform bacterium, measuring expression amount and
CC   analysing the expression profile or expression pattern of a gene derived
CC   from Coryneform bacterium, and identifying a homologue of a gene derived
CC   from coryneform bacterium. Coryneform bacteria are useful for producing
CC   amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC   particularly L-lysine. The present sequence is a nucleic acid described
CC   in the exemplification of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from the
CC   European Patent Office.
XX
SQ   Sequence 1221 BP; 272 A; 350 C; 336 G; 263 T; 0 other;

  Query Match           12.3%;  Score 29;  DB 22;  Length 1221;
  Best Local Similarity   41.0%;  Pred. No. 11;
  Matches   50;  Conservative    0;  Mismatches   72;  Indels    0;  Gaps    0;

Qy     113 ACGTACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGGTTCATCAAGA 172
           || | |||                                          |  | |    | |
Db    1067 ACCTGCGTCCAGCAGCAATTATCCGTGAGCTTGATCTGCTTCGTCCGATCTACGCTGACA 1126
```

```
Qy     173 CCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTCAAGC 232
           | || || |||||||||||||| ||    ||    ||| |  | || ||||   || | |
Db    1127 CTGCTGCCTACGGCCACTTTGGTCGCACTGATTTGGACCTTCCTTGGGAGGCTATCGACC 1186

Qy     233 CC 234
           |
Db    1187 GC 1188
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Search completed: April 23, 2003, 15:01:42
Job time : 3205.99 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 23, 2003, 12:06:28 ; Search time 19.5833 Seconds
(without alignments)
2307.226 Million cell updates/sec

Title: US-09-198-779B-1
Perfect score: 349
Sequence: 1 gttttccgtctagcctcggt.....ctgcgaggtggtcaagcccc 235

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09198779/runat_23042003_120617_2416/app_query.fasta_1.917
-DB=PIR_73 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=50
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=45 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09198779_@CGN_1_1_92_@runat_23042003_120617_2416 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	127	36.4	394	2	T06180	methionine adenosy
2	120	34.4	68	2	PQ0817	methionine adenosy
3	120	34.4	393	2	JN0131	methionine adenosy
4	120	34.4	393	2	S38875	methionine adenosy
5	120	34.4	393	2	S46538	methionine adenosy
6	120	34.4	393	2	C86155	S-adenosylmethioni
7	116	33.2	360	2	T06592	methionine adenosy
8	116	33.2	366	2	S66351	methionine adenosy
9	115	33.0	390	2	G84785	probable s-adenosy
10	115	33.0	393	2	JQ0410	methionine adenosy
11	108.5	31.1	397	2	S66352	methionine adenosy
12	101	28.9	179	2	T07899	methionine adenosy
13	101	28.9	390	2	S49491	methionine adenosy
14	101	28.9	390	2	S46540	methionine adenosy
15	98	28.1	396	2	T10710	methionine adenosy
16	74	21.2	395	2	G72228	S-adenosylmethioni
17	72	20.6	389	2	E81986	probable methionin
18	72	20.6	389	2	D81042	S-adenosylmethioni
19	68	19.5	388	2	S51671	methionine adenosy
20	65	18.6	400	2	D69657	methionine adenosy
21	64.5	18.5	407	2	B87255	S-adenosylmethioni
22	64	18.3	376	2	A82895	S-adenosylmethioni
c 23	63.5	18.4	1979	2	JW0059	mtprd protein - mo
24	63	18.1	395	1	S27257	methionine adenosy
25	63	18.1	395	2	A37118	methionine adenosy
26	63	18.1	403	2	H86976	probable S-adenosy
27	63	18.1	589	2	G87485	hypothetical prote
28	61	17.5	376	2	F90599	hypothetical prote
29	61	17.5	385	2	D71964	s-adenosylmethioni
30	61	17.5	385	2	E64544	methionine adenosy
31	61	17.5	398	2	F89964	S-adenosylmethioni
32	61	17.5	399	2	D84062	S-adenosylmethioni
33	61	17.5	399	2	F86862	methionine adenosy
34	61	17.5	399	2	AD1654	S-methionine adeno
35	61	17.5	399	2	AH1282	S-methionine adeno
36	61	17.5	403	2	F70899	probable metK prot
37	61	17.5	420	2	B97403	methionine adenosy
38	61	17.5	420	2	AB2621	S-adenosylmethioni
39	61	17.5	877	2	AC2211	heme transport pro
40	60.5	17.3	409	2	S74736	methionine adenosy
41	60	17.2	385	2	E82319	S-adenosylmethioni
c 42	60	17.3	674	2	B84381	acylaminoacyl-pept
43	59	16.9	396	2	A71281	probable S-adenosy
44	59	16.9	396	2	A47151	methionine adenosy
45	59	16.9	397	2	S06114	methionine adenosy
c 46	58.5	16.9	155	2	H89787	hypothetical prote
47	58.5	16.8	238	2	H70866	hypothetical prote
48	58	16.6	378	2	E84977	methionine adenosy
49	58	16.6	472	2	G75298	ribosomal protein
50	58	16.6	1861	2	T13845	microtubule-associ

ALIGNMENTS

RESULT 1
T06180
methionine adenosyltransferase (EC 2.5.1.6) - barley
N;Alternate names: S-adenosylmethionine synthetase
C;Species: Hordeum vulgare (barley)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 20-Jun-2000
C;Accession: T06180
R;Mori, S.
submitted to the EMBL Data Library, August 1995
A;Reference number: Z15512
A;Accession: T06180
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-394 <MOR>
A;Cross-references: EMBL:D63835; PIDN:BAA09895.1
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	2.4e-10	Length:	394
Score:	127.00	Matches:	24
Percent Similarity:	96.00%	Conservative:	0
Best Local Similarity:	96.00%	Mismatches:	1
Query Match:	36.39%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1 (1-235) x T06180 (1-394)

```
Qy    160 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362 ArgPheIleLysThrAlaAlaTyrGlyHisPheGlyArgAspAspAlaAspPheThrTrp 381

Qy    220 GAGGTGGTCAAGCCC 234
```

```
              ||||||||||||||||
Db    382 GluValValLysPro 386

RESULT 2
PQ0817
methionine adenosyltransferase (EC 2.5.1.6) - rape (fragment)
C;Species: Brassica napus (rape)
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 05-May-2000
C;Accession: PQ0817
R;Park, Y.S.; Kwak, J.M.; Kwon, O.Y.; Kim, Y.S.; Lee, D.S.; Cho, M.J.; Lee, H.H.; Nam, H
Plant Physiol. 103, 359-370, 1993
A;Title: Generation of expressed sequence tags of random root cDNA clones of Brassica na
A;Reference number: PQ0816; MUID:94302145; PMID:8029332
A;Accession: PQ0817
A;Molecule type: mRNA
A;Residues: 1-68 <PAR>
A;Experimental source: root, cv. Naehan
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:              2.54e-09        Length:         68
Score:                  120.00          Matches:        22
Percent Similarity:     92.00%          Conservative:   1
Best Local Similarity:  88.00%          Mismatches:     2
Query Match:            34.38%          Indels:         0
DB:                     2               Gaps:           0

US-09-198-779B-1 (1-235) x PQ0817 (1-68)

Qy    160 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 219
          ||||||:::||||||||||||||||||||||||||||||||||||   |||||||||
Db     36 ArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrp 55

Qy    220 GAGGTGGTCAAGCCC 234
          |||||||||||||||
Db     56 GluValValLysPro 60

RESULT 3
JN0131
methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana
N;Alternate names: S-adenosylmethionine synthetase
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 05-May-2000
C;Accession: JN0131
R;Peleman, J.; Boerjan, W.; Engler, G.; Seurinck, J.; Botterman, J.; Alliotte, T.; Van M
Plant Cell 1, 81-93, 1989
A;Title: Strong cellular preference in the expression of a housekeeping gene of Arabidop
A;Reference number: JN0131; MUID:92386056; PMID:2535470
A;Accession: JN0131
A;Molecule type: DNA
A;Residues: 1-393 <PEL>
A;Cross-references: GB:M55077; NID:g166871; PIDN:AAA32868.1; PID:g166872
A;Experimental source: var. K85
A;Note: the sequence derived from var. Columbia differs from that shown in having 117-Gl
A;Note: the authors translated the codon GAC for residue 117 as Glu
C;Comment: S-Adenosylmethionine synthetase catalyzes the biosysnthesis of adenosylmethic
C;Genetics:
A;Gene: sam-1
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:              2.76e-09        Length:         393
Score:                  120.00          Matches:        22
Percent Similarity:     92.00%          Conservative:   1
Best Local Similarity:  88.00%          Mismatches:     2
Query Match:            34.38%          Indels:         0
DB:                     2               Gaps:           0

US-09-198-779B-1 (1-235) x JN0131 (1-393)

Qy    160 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 219
          ||||||:::||||||||||||||||||||||||||||||||||||   |||||||||
Db    361 ArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrp 380

Qy    220 GAGGTGGTCAAGCCC 234
          |||||||||||||||
Db    381 GluValValLysPro 385

RESULT 4
S38875
methionine adenosyltransferase (EC 2.5.1.6) - tomato
N;Alternate names: S-adenosyl-L-methionine synthetase
C;Species: Lycopersicon esculentum (tomato)
C;Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
C;Accession: S46539; S38875
R;Espartero, J.; Pintor-Toro, J.A.; Pardo, J.M.
Plant Mol. Biol. 25, 217-227, 1994
A;Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in
A;Reference number: S46538; MUID:94289646; PMID:8018871
A;Accession: S46539
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-393 <ES2>
A;Cross-references: EMBL:Z24742; NID:g429105; PIDN:CAA80866.1; PID:g429106
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:              2.76e-09        Length:         393
Score:                  120.00          Matches:        22
Percent Similarity:     92.00%          Conservative:   1
Best Local Similarity:  88.00%          Mismatches:     2
Query Match:            34.38%          Indels:         0
DB:                     2               Gaps:           0

US-09-198-779B-1 (1-235) x S38875 (1-393)

Qy    160 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 219
          ||||||:::||||||||||||||||||||||||||||||||||||   |||||||||
Db    361 ArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrp 380

Qy    220 GAGGTGGTCAAGCCC 234
          |||||||||||||||
Db    381 GluValValLysPro 385

RESULT 5
S46538
methionine adenosyltransferase (EC 2.5.1.6) - tomato
N;Alternate names: S-adenosyl-L-methionine synthetase
C;Species: Lycopersicon esculentum (tomato)
C;Date: 26-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
C;Accession: S46538; S38874
R;Espartero, J.; Pintor-Toro, J.A.; Pardo, J.M.
Plant Mol. Biol. 25, 217-227, 1994
A;Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in
A;Reference number: S46538; MUID:94289646; PMID:8018871
A;Accession: S46538
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-393 <ESP>
A;Cross-references: EMBL:Z24741; NID:g429103; PIDN:CAA80865.1; PID:g429104
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:              2.76e-09        Length:         393
Score:                  120.00          Matches:        22
Percent Similarity:     92.00%          Conservative:   1
Best Local Similarity:  88.00%          Mismatches:     2
Query Match:            34.38%          Indels:         0
DB:                     2               Gaps:           0

US-09-198-779B-1 (1-235) x S46538 (1-393)
```

```
Qy     160 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 219
           ||||||:::||||||||||||||||||||||||||||||||||||   |||||||||
Db     361 ArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrp 380

Qy     220 GAGGTGGTCAAGCCC 234
           |||||||||||||||
Db     381 GluValValLysPro 385
```

RESULT 6
C86155
S-adenosylmethionine synthetase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C86155
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C86155
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-393 <STO>
A;Cross-references: GB:AE005172; NID:g9972389; PIDN:AAG10639.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	2.76e-09	Length:	393
Score:	120.00	Matches:	22
Percent Similarity:	92.00%	Conservative:	1
Best Local Similarity:	88.00%	Mismatches:	2
Query Match:	34.38%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1 (1-235) x C86155 (1-393)

```
Qy     160 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 219
           ||||||:::||||||||||||||||||||||||||||||||||||   |||||||||
Db     361 ArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrp 380

Qy     220 GAGGTGGTCAAGCCC 234
           |||||||||||||||
Db     381 GluValValLysPro 385
```

RESULT 7
T06592
methionine adenosyltransferase (EC 2.5.1.6) - garden pea (fragment)
C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C;Accession: T06592
R;Gomez, L.; Carrasco, P.
submitted to the EMBL Data Library, January 1995
A;Description: Hormonal regulation of the S-adenosylmethionine synthase in pea ovaries.
A;Reference number: Z15782
A;Accession: T06592
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-360 <GOM>
A;Cross-references: EMBL:L36680; NID:g609556; PIDN:AAA58772.1; PID:g609557
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	1.11e-08	Length:	360
Score:	116.00	Matches:	21
Percent Similarity:	92.00%	Conservative:	2
Best Local Similarity:	84.00%	Mismatches:	2
Query Match:	33.24%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1 (1-235) x T06592 (1-360)

```
Qy     160 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 219
           ||||||:::|||||||||||||||||||||||||||||||:::|||   |||||||||
Db     330 ArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrp 349

Qy     220 GAGGTGGTCAAGCCC 234
           |||||||||||||||
Db     350 GluValValLysPro 354
```

RESULT 8
S66351
methionine adenosyltransferase (EC 2.5.1.6) 1 - garden pea (fragment)
C;Species: Pisum sativum (garden pea)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-May-2000
C;Accession: S66351
R;Gomez-Gomez, L.; Carrasco, P.
Plant Mol. Biol. 30, 821-832, 1996
A;Title: Hormonal regulation of S-adenosylmethionine synthase transcripts in pea ovar
A;Reference number: S66351; MUID:96194463; PMID:8624412
A;Accession: S66351
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-366 <GOM>
A;Cross-references: EMBL:X82076; NID:g609222; PIDN:CAA57580.1; PID:g609223
A;Note: the authors did not translate the codon for residue 1
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	1.11e-08	Length:	366
Score:	116.00	Matches:	21
Percent Similarity:	92.00%	Conservative:	2
Best Local Similarity:	84.00%	Mismatches:	2
Query Match:	33.24%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1 (1-235) x S66351 (1-366)

```
Qy     160 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 219
           ||||||:::|||||||||||||||||||||||||||||||:::|||   |||||||||
Db     336 ArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrp 355

Qy     220 GAGGTGGTCAAGCCC 234
           |||||||||||||||
Db     356 GluValValLysPro 360
```

RESULT 9
G84785
probable s-adenosylmethionine synthetase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: G84785
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84785
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-390 <STO>
A;Cross-references: GB:AE002093; NID:g4883604; PIDN:AAD31573.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g36880
A;Map position: 2
C;Superfamily: methionine adenosyltransferase

```
Alignment Scores:
Pred. No.:              1.58e-08        Length:         390
Score:                  115.00          Matches:        22
Percent Similarity:     88.00%          Conservative:   0
Best Local Similarity:  88.00%          Mismatches:     3
Query Match:            32.95%          Indels:         0
DB:                     2               Gaps:           0

US-09-198-779B-1 (1-235) x G84785 (1-390)

Qy    160 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 219
          ||||||   ||||||||||||||||||||||||||||||||||||   |||||||||
Db    361 ArgPheGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrp 380

Qy    220 GAGGTGGTCAAGCCC 234
          |||||||||||||||
Db    381 GluValValLysPro 385

RESULT 10
JQ0410
methionine adenosyltransferase (EC 2.5.1.6) 2 - Arabidopsis thaliana
N;Alternate names: S-adenosylmethionine synthetase
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-May-2000
C;Accession: JQ0410
R;Peleman, J.; Saito, K.; Cottyn, B.; Engler, G.; Seurinck, J.; Van Montagu, M.; Inze, D
Gene 84, 359-369, 1989
A;Title: Structure and expression analyses of the S-adenosylmethionine synthetase gene f
A;Reference number: JQ0410; MUID:90128280; PMID:2482229
A;Accession: JQ0410
A;Molecule type: DNA
A;Residues: 1-393 <PEL>
A;Cross-references: GB:M33217; NID:g166873; PIDN:AAA32869.1; PID:g166874
C;Genetics:
A;Gene: sam-2
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:              1.58e-08        Length:         393
Score:                  115.00          Matches:        22
Percent Similarity:     88.00%          Conservative:   0
Best Local Similarity:  88.00%          Mismatches:     3
Query Match:            32.95%          Indels:         0
DB:                     2               Gaps:           0

US-09-198-779B-1 (1-235) x JQ0410 (1-393)

Qy    160 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 219
          ||||||   ||||||||||||||||||||||||||||||||||||   |||||||||
Db    361 ArgPheGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrp 380

Qy    220 GAGGTGGTCAAGCCC 234
          |||||||||||||||
Db    381 GluValValLysPro 385

RESULT 11
S66352
methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-May-2000
C;Accession: S66352; S52218
R;Gomez-Gomez, L.; Carrasco, P.
Plant Mol. Biol. 30, 821-832, 1996
A;Title: Hormonal regulation of S-adenosylmethionine synthase transcripts in pea ovaries
A;Reference number: S66351; MUID:96194463; PMID:8624412
A;Accession: S66352
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-397 <GOM>
A;Cross-references: EMBL:X82077
R;Gomez, L.; Carrasco, P.
submitted to the EMBL Data Library, October 1994
A;Description: Hormonal regulation of the s-adenosylmethionine synthase in pea ovarie
A;Reference number: S52218
A;Accession: S52218
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-364,'FEDSCIWTFW' <GOW>
A;Cross-references: EMBL:X82077; NID:g609224; PIDN:CAA57581.1; PID:g609225
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:              1.53e-07        Length:         397
Score:                  108.50          Matches:        22
Percent Similarity:     88.46%          Conservative:   1
Best Local Similarity:  84.62%          Mismatches:     2
Query Match:            31.09%          Indels:         1
DB:                     2               Gaps:           1

US-09-198-779B-1 (1-235) x S66352 (1-397)

Qy    160 AGGTTC---ATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACC 216
          ||||||   :::||||||||||||||||||||||||||   ||||||||||||||||||
Db    363 ArgPheLeuLeuLysThrAlaAlaTyrGlyHisPheGlySerAspAspAlaAspPheThr 382

Qy    217 TGCGAGGTGGTCAAGCCC 234
              ||||||||||||||||
Db    383 TrpGluValValLysPro 388

RESULT 12
T07899
methionine adenosyltransferase (EC 2.5.1.6) - Chlamydomonas reinhardtii (fragment)
N;Alternate names: S-adenosylmethionine synthetase
C;Species: Chlamydomonas reinhardtii
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 05-May-2000
C;Accession: T07899
R;Kim, J.Y.; Lee, K.O.; Lee, S.H.
submitted to the EMBL Data Library, June 1997
A;Description: Chlamydomonas reinhardtii mRNA for S-adenosylmethionine synthetase.
A;Reference number: Z16198
A;Accession: T07899
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-179 <KIM>
A;Cross-references: EMBL:AF008568; NID:g2454483; PIDN:AAB71833.1; PID:g2454484
A;Experimental source: strain 137C
C;Genetics:
A;Gene: SAMS
C;Function:
A;Description: catalyzes the formation of S-adenosyl methionine with phosphate and py
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:              2.02e-06        Length:         179
Score:                  101.00          Matches:        19
Percent Similarity:     83.33%          Conservative:   1
Best Local Similarity:  79.17%          Mismatches:     4
Query Match:            28.94%          Indels:         0
DB:                     2               Gaps:           0

US-09-198-779B-1 (1-235) x T07899 (1-179)

Qy    160 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 219
          |||:::   ||||||||||||||||||||||||||||||||||||   |||||||||
Db    153 ArgTyrGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrp 172

Qy    220 GAGGTGGTCAAG 231
          |||   ||||||
Db    173 GluThrValLys 176

RESULT 13
S49491
```

```
methionine adenosyltransferase (EC 2.5.1.6) - garden petunia
C;Species: Petunia x hybrida (garden petunia)
C;Date: 01-Feb-1995 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
C;Accession: S49491
R;Izhaki, A.; Shoseyov, O.; Weiss, D.
submitted to the EMBL Data Library, October 1994
A;Description: Petunia cDNA encoding S-Adenosylmethionine synthetase.
A;Reference number: S49491
A;Accession: S49491
A;Molecule type: mRNA
A;Residues: 1-390 <IZH>
A;Cross-references: EMBL:X82214; NID:g559505; PIDN:CAA57696.1; PID:g559506
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:                2.1e-06        Length:          390
Score:                    101.00         Matches:         19
Percent Similarity:       83.33%         Conservative:    1
Best Local Similarity:    79.17%         Mismatches:      4
Query Match:              28.94%         Indels:          0
DB:                       2              Gaps:            0

US-09-198-779B-1 (1-235) x S49491 (1-390)

Qy     160 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 219
           |||:::   |||||||||||||||||||||||||||||||||||||   |||||||||
Db     361 ArgTyrGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrp 380

Qy     220 GAGGTGGTCAAG 231
           |||   ||||||
Db     381 GluThrValLys 384

RESULT 14
S46540
methionine adenosyltransferase (EC 2.5.1.6) - tomato
N;Alternate names: S-adenosyl-L-methionine synthetase
C;Species: Lycopersicon esculentum (tomato)
C;Date: 26-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
C;Accession: S46540; S38876
R;Espartero, J.; Pintor-Toro, J.A.; Pardo, J.M.
Plant Mol. Biol. 25, 217-227, 1994
A;Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in res
A;Reference number: S46538; MUID:94289646; PMID:8018871
A;Accession: S46540
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-390 <ESP>
A;Cross-references: EMBL:Z24743; NID:g429107; PIDN:CAA80867.1; PID:g429108
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:                2.1e-06        Length:          390
Score:                    101.00         Matches:         19
Percent Similarity:       83.33%         Conservative:    1
Best Local Similarity:    79.17%         Mismatches:      4
Query Match:              28.94%         Indels:          0
DB:                       2              Gaps:            0

US-09-198-779B-1 (1-235) x S46540 (1-390)

Qy     160 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 219
           |||:::   |||||||||||||||||||||||||||||||||||||   |||||||||
Db     361 ArgTyrGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrp 380

Qy     220 GAGGTGGTCAAG 231
           |||   ||||||
Db     381 GluThrValLys 384

RESULT 15
T10710
methionine adenosyltransferase (EC 2.5.1.6) - clove pink
N;Alternate names: S-adenosylmethionine synthetase
C;Species: Dianthus caryophyllus (clove pink)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-May-2000
C;Accession: T10710
R;Larsen, P.B.; Woodson, W.R.
submitted to the EMBL Data Library, April 1991
A;Description: Cloning and nucleotide sequence of a s-adenosylmethionine synthetase c
A;Reference number: Z17091
A;Accession: T10710
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-396 <LAR>
A;Cross-references: EMBL:M61882; NID:g167961; PID:g304637
C;Genetics:
A;Gene: SAM2
C;Function:
A;Description: catalyzes the formation of S-adenosyl methionine with phosphate and py
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:                5.98e-06       Length:          396
Score:                    98.00          Matches:         17
Percent Similarity:       83.33%         Conservative:    3
Best Local Similarity:    70.83%         Mismatches:      4
Query Match:              28.08%         Indels:          0
DB:                       2              Gaps:            0

US-09-198-779B-1 (1-235) x T10710 (1-396)

Qy     160 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 219
           |||::::::|||||||||||||||||||||||||||||||:::|||   |||||||||
Db     364 ArgTyrLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrp 383

Qy     220 GAGGTGGTCAAG 231
           |||      |||
Db     384 GluAlaAlaLys 387

RESULT 16
G72228
S-adenosylmethionine synthetase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: G72228
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
 C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: G72228
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-395 <ARN>
A;Cross-references: GB:AE001807; GB:AE000512; NID:g4982216; PIDN:AAD36725.1; PID:g498
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1658
C;Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.:                0.026          Length:          395
Score:                    74.00          Matches:         13
Percent Similarity:       88.89%         Conservative:    3
Best Local Similarity:    72.22%         Mismatches:      2
Query Match:              21.20%         Indels:          0
DB:                       2              Gaps:            0

US-09-198-779B-1 (1-235) x G72228 (1-395)

Qy     169 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 222
           |||||||||||||||||||||||||||||::::::   :::|||||||   |||
Db     364 LysThrAlaAlaTyrGlyHisPheGlyArgAsnGluGluGluPheThrTrpGlu 381
```

RESULT 17
E81986
probable methionine adenosyltransferase (EC 2.5.1.6) NMA0663 [imported] - Neisseria meni
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: E81986
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: E81986
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 <PAR>
A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83950.1; PID:g737939
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: metK; NMA0663
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	0.0523	Length:	389
Score:	72.00	Matches:	12
Percent Similarity:	85.00%	Conservative:	5
Best Local Similarity:	60.00%	Mismatches:	3
Query Match:	20.63%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1 (1-235) x E81986 (1-389)

```
Qy    163 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 222
          :::   |||:::|||||||||||||||||||||||||||::::::   :::||||||   |||
Db    356 TyrSerLysSerAlaAlaTyrGlyHisPheGlyArgGluGluProGluPheThrTrpGlu 375
```

RESULT 18
D81042
S-adenosylmethionine synthetase NMB1799 [imported] - Neisseria meningitidis (strain MC58
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: D81042
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: D81042
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 <TET>
A;Cross-references: GB:AE002530; GB:AE002098; NID:g7227054; PIDN:AAF42136.1; PID:g722705
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1799
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	0.0523	Length:	389
Score:	72.00	Matches:	12
Percent Similarity:	85.00%	Conservative:	5
Best Local Similarity:	60.00%	Mismatches:	3
Query Match:	20.63%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1 (1-235) x D81042 (1-389)

```
Qy    163 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 222
          :::   |||:::|||||||||||||||||||||||||||::::::   :::||||||   |||
Db    356 TyrSerLysSerAlaAlaTyrGlyHisPheGlyArgGluGluProGluPheThrTrpGlu 375
```

RESULT 19
S51671
methionine adenosyltransferase (EC 2.5.1.6) - Acanthamoeba castellanii
C;Species: Acanthamoeba castellanii
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 05-May-2000
C;Accession: S51671
R;Ahn, K.S.; Henney, H.
submitted to the EMBL Data Library, May 1994
A;Reference number: S51671
A;Accession: S51671
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-388 <AHN>
A;Cross-references: EMBL:X79205
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	0.211	Length:	388
Score:	68.00	Matches:	13
Percent Similarity:	71.43%	Conservative:	2
Best Local Similarity:	61.90%	Mismatches:	6
Query Match:	19.48%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1 (1-235) x S51671 (1-388)

```
Qy    169 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTC 228
          |||||||||   :::|||||||||||||||||:::|||   ||||||      |||
Db    364 LysThrAlaTyrHisGlyHisPheGlyArgAsnAspProAspPheLeuTrpGluAlaPro 383

Qy    229 AAG 231
          |||
Db    384 Lys 384
```

RESULT 20
D69657
methionine adenosyltransferase (EC 2.5.1.6) - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: D69657
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: D69657
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-400 <KUN>
A;Cross-references: GB:Z99119; GB:AL009126; NID:g2635411; PIDN:CAB15033.1; PID:g26355
A;Experimental source: strain 168
C;Genetics:
A;Gene: metK
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	0.603	Length:	400
Score:	65.00	Matches:	12
Percent Similarity:	72.22%	Conservative:	1

```
Best Local Similarity:  66.67%          Mismatches:     5
Query Match:            18.62%          Indels:         0
DB:                     2               Gaps:           0

US-09-198-779B-1 (1-235) x D69657 (1-400)

Qy    169 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 222
          :::|||||||||||||||||||||||||||   |||   |||         |||
Db    368 GlnThrAlaAlaTyrGlyHisPheGlyArgHisAspValAspLeuProTrpGlu 385

RESULT 21
B87255
S-adenosylmethionine synthetase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: B87255
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: B87255
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-407 <STO>
A;Cross-references: GB:AE005673; NID:g13421144; PIDN:AAK22038.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC0050
C;Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.:              0.718           Length:         407
Score:                  64.50           Matches:        20
Percent Similarity:     43.06%          Conservative:   11
Best Local Similarity:  27.78%          Mismatches:     18
Query Match:            18.48%          Indels:         23
DB:                     2               Gaps:           3

US-09-198-779B-1 (1-235) x B87255 (1-407)

Qy     16 TCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGT 75
          :::|||          |||||||||   ||||||   |||   :::          :::|||
Db    344 AlaValLeuGluLysThrLeuProGlnLeuIleGlyGlyAlaThrProArgAlaIleArg 363

Qy     76 TGTGTTATTAATGTTGTATAATTGAGCAGGACACAACACGTACGTTNNNNNNNNNNNNNN 135
                                       :::|||::::::
Db    364 --------------------------------GluHisLeuGlnLeuAsnArgProIle 372

Qy    136 NNNNNNNNNNNNNNNNNNNNNNCAGGTTCATCAAGACCGCCGCATACGGCCACTTTGGC 195
                                  :::   :::||||||||||||||||||||||||
Db    373 --------------------------TyrAlaArgThrAlaAlaTyrGlyHisPheGly 383

Qy    196 CGT---------GACGACGCCGACTTCACCTGCGAG 222
          |||         ::::::      |||:::   |||
Db    384 ArgThrProAspAsnGluGlyGlyPheSerTrpGlu 395

RESULT 22
A82895
S-adenosylmethionine synthetase UU412 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: A82895
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mi
A;Reference number: A82870
A;Accession: A82895
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <GLA>
A;Cross-references: GB:AE002138; GB:AF222894; NID:g6899390; PIDN:AAF30823.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: metK; UU412
A;Genetic code: SGC3
C;Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.:              0.852           Length:         376
Score:                  64.00           Matches:        10
Percent Similarity:     71.43%          Conservative:   5
Best Local Similarity:  47.62%          Mismatches:     6
Query Match:            18.34%          Indels:         0
DB:                     2               Gaps:           0

US-09-198-779B-1 (1-235) x A82895 (1-376)

Qy    160 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 219
          :::::::::      |||   ||||||||||||||||||||||   :::   :::
Db    343 LysTyrLeuProValAlaThrTyrGlyHisPheGlyArgAspAspLeuAsnLeuSerTrp 362

Qy    220 GAG 222
          |||
Db    363 Glu 363

RESULT 23
JW0059
mtprd protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 02-Aug-2002
C;Accession: JW0059
R;Tsukahara, F.; Urakawa, I.; Hattori, M.; Hirai, M.; Ohba, K.; Yoshioka, T.; Sakaki,
J. Biochem. 123, 1055-1063, 1998
A;Title: Molecular characterization of the mouse mtprd gene, a homologue of human TPR
A;Reference number: JW0059; MUID:98269034; PMID:9603993
A;Accession: JW0059
A;Molecule type: protein
A;Residues: 1-1979 <TSU>
C;Comment: This protein has three units of tetratrics-peptide repeats.
C;Genetics:
A;Gene: mtprd
A;Map position: 16C3.3-4
C;Superfamily: mtprd protein; tetratricopeptide repeat homology
F;1927-1976/Domain: RING finger homology <RRN>

Alignment Scores:
Pred. No.:              1.1             Length:         1979
Score:                  63.50           Matches:        20
Percent Similarity:     36.59%          Conservative:   10
Best Local Similarity:  24.39%          Mismatches:     37
Query Match:            18.35%          Indels:         15
DB:                     2               Gaps:           2

US-09-198-779B-1 (1-235) x JW0059 (1-1979)

Qy    228 GACCACCTCGCAGGTGAAGTCGGCGTCGTCACGGCCAAAGTGGCCGTATGC--------- 178
          ||||||:::|||   |||      ::::::         :::   ||||||
Db   1382 AspHisMetAlaSerGluThrGlnIleLeuGluAspThrLeuGlyValCysValArgSer 1401

Qy    177 ------------------------GGCGGTCTTGATGAACCTGNNNNNNNNNNNNNNNN 142
                                     |||   ||||||
Db   1402 GlnGlySerAlaAlaAspAlaAspProAlaLeuSerGluProGluGlyAsnSerGluHis 1421

Qy    141 NNNNNNNNNNNNNNNNNNNNNAACGTACGTGTTGTGTCCTGCTCAATTATACAACATTAAT 82
                                      |||      |||   |||   |||::::::
Db   1422 SerGlySerSerAspSer-----------LeuTrpGluAlaSerLeuGluAsnValSer 1437

Qy     81 AACACAACGAACAATGGATCAGGACCGTCCATTTATCAGCATGGGCAGCGTCGATCTGTC 22
             ||||||:::      :::   |||||||:::               |||      |||
Db   1438 GlyThrThrAspAlaProAlaAlaProSerValAlaIleGlnValSerArgSerMetVal 1457

Qy     21 CACCGA 16
          |||:::
Db   1458 HisGln 1459
```

RESULT 24
S27257
methionine adenosyltransferase (EC 2.5.1.6) 2 alpha chain - human
N;Alternate names: renal methionine adenosyltransferase (MAT); S-adenosylmethionine synt
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 11-Jun-1999
C;Accession: S27257
R;Horikawa, S.; Tsukada, K.
FEBS Lett. 312, 37-41, 1992
A;Title: Molecular cloning and developmental expression of a human kidney S-adenosylmeth
A;Reference number: S27257; MUID:93050159; PMID:1426236
A;Accession: S27257
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-395 <HOR>
A;Cross-references: EMBL:X68836; GB:S47859; NID:g36326; PIDN:CAA48726.1; PID:g36327
C;Genetics:
A;Gene: GDB:MAT2A; SAMS2; MATA2
A;Cross-references: GDB:136213; OMIM:601468
A;Map position: 2p11.2-2p11.2
A;Introns: 15/2; 256/3
C;Complex: heterodimer of catalytic alpha and regulatory beta chains
C;Function:
A;Description: catalyzes the formation of S-adenosyl methionine with phosphate and pyrop
A;Pathway: one-carbon metabolism
C;Superfamily: methionine adenosyltransferase
C;Keywords: ATP; heterodimer; kidney; magnesium; metalloprotein; one-carbon metabolism;
F;279-286/Region: nucleotide-binding motif A (P-loop) #status atypical
F;31/Binding site: magnesium 2 (Asp) #status predicted
F;285,289/Active site: Lys #status predicted
F;291/Binding site: magnesium 1 (Asp) #status predicted

Alignment Scores:

Pred. No.:	1.21	Length:	395
Score:	63.00	Matches:	14
Percent Similarity:	71.43%	Conservative:	1
Best Local Similarity:	66.67%	Mismatches:	4
Query Match:	18.05%	Indels:	2
DB:	1	Gaps:	1

US-09-198-779B-1 (1-235) x S27257 (1-395)

```
Qy    169 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTC 228
          :::||||||||||||||||||||||||||||||         |||      ||||||
Db    373 ArgThrAlaAlaTyrGlyHisPheGlyArgAsp------SerPheProTrpGluValPro 390

Qy    229 AAG 231
          |||
Db    391 Lys 391
```

RESULT 25
A37118
methionine adenosyltransferase (EC 2.5.1.6) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 05-May-2000
C;Accession: A37118
R;Horikawa, S.; Sasuga, J.; Shimizu, K.; Ozasa, H.; Tsukada, K.
J. Biol. Chem. 265, 13683-13686, 1990
A;Title: Molecular cloning and nucleotide sequence of cDNA encoding the rat kidney S-ade
A;Reference number: A37118; MUID:90337979; PMID:1696256
A;Accession: A37118
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-395 <HOR>
A;Cross-references: GB:J05571; NID:g206845; PIDN:AAA42106.1; PID:g206846
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	1.21	Length:	395
Score:	63.00	Matches:	14
Percent Similarity:	71.43%	Conservative:	1
Best Local Similarity:	66.67%	Mismatches:	4
Query Match:	18.05%	Indels:	2
DB:	2	Gaps:	1

US-09-198-779B-1 (1-235) x A37118 (1-395)

```
Qy    169 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTC 228
          :::||||||||||||||||||||||||||||||         |||      ||||||
Db    373 ArgThrAlaAlaTyrGlyHisPheGlyArgAsp------SerPheProTrpGluValPro 390

Qy    229 AAG 231
          |||
Db    391 Lys 391
```

RESULT 26
H86976
probable S-adenosylmethionine synthase [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: H86976
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holro
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: H86976
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-403 <STO>
A;Cross-references: GB:AL450380; NID:g13092748; PIDN:CAC30052.1; GSPDB:GN00147
C;Genetics:
A;Gene: metK
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	1.21	Length:	403
Score:	63.00	Matches:	11
Percent Similarity:	70.00%	Conservative:	3
Best Local Similarity:	55.00%	Mismatches:	6
Query Match:	18.05%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1 (1-235) x H86976 (1-403)

```
Qy    163 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 222
          :::   :::||||||||||||||||||||||||||||   |||   :::         |||
Db    372 TyrAlaGlnThrAlaAlaTyrGlyHisPheGlyArgThrAspValGluLeuProTrpGlu 391
```

RESULT 27
G87485
hypothetical protein CC1908 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: G87485
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87485
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-589 <STO>
A;Cross-references: GB:AE005673; NID:g13423359; PIDN:AAK23883.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC1908

Alignment Scores:

Pred. No.:	1.23	Length:	589
Score:	63.00	Matches:	19
Percent Similarity:	36.07%	Conservative:	3

```
Best Local Similarity:  31.15%          Mismatches:     27
Query Match:            18.05%          Indels:         12
DB:                     2               Gaps:           2

US-09-198-779B-1 (1-235) x G87485 (1-589)

Qy      53 GACGGTCCTGATCCATTGTTCGTTGTGTTATTAATGTTGTATAATTGAGCAGGACACAAC 112
           ||||||||||||||||                                        |||
Db     240 AspGlyProAspPro--------------------------------GlnGlyProMet 248

Qy     113 ACGTACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGGTTCATCAAGA 172
           |||:::                                                  ||||||
Db     249 ThrHisGlnAlaArgAlaAsnGlySerSerSerSerAlaGlyAlaMetAlaSerSer--- 267

Qy     173 CCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTCAAGC 232
           ||||||      :::   ||||||         |||   :::||||||      ||||||
Db     268 ProProAlaGlnSerArgLeuAlaAlaAspAlaProAspAlaProAlaAlaThrSerSer 287

Qy     233 CCC 235
           |||
Db     288 Pro 288

RESULT 28
F90599
hypothetical protein MYPU_7020 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: F90599
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: F90599
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <KUR>
A;Cross-references: GB:AL445566; PID:g14090117; PIDN:CAC13875.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPU_7020
A;Genetic code: SGC3
C;Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.:              2.43            Length:         376
Score:                  61.00           Matches:        10
Percent Similarity:     66.67%          Conservative:   4
Best Local Similarity:  47.62%          Mismatches:     7
Query Match:            17.48%          Indels:         0
DB:                     2               Gaps:           0

US-09-198-779B-1 (1-235) x F90599 (1-376)

Qy     160 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 219
           ::::::      |||:::   :::||||||||||||||||||||   |||
Db     343 LysTyrPheProThrSerPhePheGlyHisPheGlyArgAspAspLeuAspLeuProTrp 362

Qy     220 GAG 222
           |||
Db     363 Glu 363

RESULT 29
D71964
s-adenosylmethionine synthetase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 18-Jun-1999
C;Accession: D71964
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: D71964
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-385 <ARN>
A;Cross-references: GB:AE001456; GB:AE001439; NID:g4154689; PIDN:AAD05755.1; PID:g415
A;Experimental source: strain J99
C;Genetics:
A;Gene: metK
C;Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.:              2.43            Length:         385
Score:                  61.00           Matches:        11
Percent Similarity:     82.35%          Conservative:   3
Best Local Similarity:  64.71%          Mismatches:     3
Query Match:            17.48%          Indels:         0
DB:                     2               Gaps:           0

US-09-198-779B-1 (1-235) x D71964 (1-385)

Qy     172 ACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 222
           |||:::|||||||||||||||||||||:::      :::||||||   |||
Db     355 ThrSerAlaTyrGlyHisPheGlyArgGluLeuGluGluPheThrTrpGlu 371

RESULT 30
E64544
methionine adenosyltransferase (EC 2.5.1.6) 2 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 05-May-2000
C;Accession: E64544
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKe
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: E64544
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-385 <TOM>
A;Cross-references: GB:AE000540; GB:AE000511; NID:g2313287; PIDN:AAD07267.1; PID:g231
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:              2.43            Length:         385
Score:                  61.00           Matches:        11
Percent Similarity:     82.35%          Conservative:   3
Best Local Similarity:  64.71%          Mismatches:     3
Query Match:            17.48%          Indels:         0
DB:                     2               Gaps:           0

US-09-198-779B-1 (1-235) x E64544 (1-385)

Qy     172 ACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 222
           |||:::|||||||||||||||||||||:::      :::||||||   |||
Db     355 ThrSerAlaTyrGlyHisPheGlyArgGluLeuGluGluPheThrTrpGlu 371

RESULT 31
F89964
S-adenosylmethionine synthetase [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: F89964
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: F89964
A;Status: preliminary
```

A;Molecule type: DNA
A;Residues: 1-398 <KUR>
A;Cross-references: GB:BA000018; PID:g13701583; PIDN:BAB42876.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: metK
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	2.43	Length:	398
Score:	61.00	Matches:	12
Percent Similarity:	72.22%	Conservative:	1
Best Local Similarity:	66.67%	Mismatches:	5
Query Match:	17.48%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1 (1-235) x F89964 (1-398)

```
Qy    169 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 222
          :::||||||||||||||||||||||||||||   |||    |||      |||
Db    367 GlnThrAlaAlaTyrGlyHisPheGlyArgThrAspValLeuPheProTrpGlu 384
```

RESULT 32
D84062
S-adenosylmethionine synthetase metK [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: D84062
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D84062
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-399 <STO>
A;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB07019.1; GSPDB:GN0
A;Experimental source: strain C-125
C;Genetics:
A;Gene: metK
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	2.43	Length:	399
Score:	61.00	Matches:	11
Percent Similarity:	72.22%	Conservative:	2
Best Local Similarity:	61.11%	Mismatches:	5
Query Match:	17.48%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1 (1-235) x D84062 (1-399)

```
Qy    169 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 222
          :::||||||||||||||||||||||||||||   |||    :::      |||
Db    370 GlnThrAlaAlaTyrGlyHisPheGlyArgThrAspValGluLeuProTrpGlu 387
```

RESULT 33
F86862
methionine adenosyltransferase (EC 2.5.1.6) [imported] - Lactococcus lactis subsp. lacti
N;Alternate names: S-adenosylmethionine synthetase
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: F86862
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: F86862
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-399 <STO>
A;Cross-references: GB:AE005176; PID:g12724937; PIDN:AAK06000.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: metK
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	2.43	Length:	399
Score:	61.00	Matches:	11
Percent Similarity:	72.22%	Conservative:	2
Best Local Similarity:	61.11%	Mismatches:	5
Query Match:	17.48%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1 (1-235) x F86862 (1-399)

```
Qy    169 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 222
          :::||||||||||||||||||||||||||||   |||    :::      |||
Db    368 GlnThrAlaAlaTyrGlyHisPheGlyArgThrAspValGluLeuProTrpGlu 385
```

RESULT 34
AD1654
S-methionine adenosyltransferase homolog metK [imported] - Listeria innocua (strain C
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AD1654
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1654
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-399 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC97004.1; PID:g16414260; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: metK
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	2.43	Length:	399
Score:	61.00	Matches:	11
Percent Similarity:	72.22%	Conservative:	2
Best Local Similarity:	61.11%	Mismatches:	5
Query Match:	17.48%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1 (1-235) x AD1654 (1-399)

```
Qy    169 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 222
          :::||||||||||:::|||||||||||||||||   |||    |||      |||
Db    368 GlnThrAlaAlaPheGlyHisPheGlyArgSerAspLeuAspLeuProTrpGlu 385
```

RESULT 35
AH1282
S-methionine adenosyltransferase homolog metK [imported] - Listeria monocytogenes (st
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AH1282
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1282
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-399 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC99742.1; PID:g16411100; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: metK
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	2.43	Length:	399
Score:	61.00	Matches:	11
Percent Similarity:	72.22%	Conservative:	2
Best Local Similarity:	61.11%	Mismatches:	5
Query Match:	17.48%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1 (1-235) x AH1282 (1-399)

```
Qy    169 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 222
          :::||||||||||:::|||||||||||||||   |||   |||         |||
Db    368 GlnThrAlaAlaPheGlyHisPheGlyArgSerAspLeuAspLeuProTrpGlu 385
```

RESULT 36
F70899
probable metK protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: F70899
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70899
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-403 <COL>
A;Cross-references: GB:Z80108; GB:AL123456; NID:g3256012; PIDN:CAB02194.1; PID:g3256013
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: metK
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	2.44	Length:	403
Score:	61.00	Matches:	11
Percent Similarity:	65.00%	Conservative:	2
Best Local Similarity:	55.00%	Mismatches:	7
Query Match:	17.48%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1 (1-235) x F70899 (1-403)

```
Qy    163 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 222
          :::      ||||||||||||||||||||||||||||   |||   :::         |||
Db    372 TyrAlaProThrAlaAlaTyrGlyHisPheGlyArgThrAspValGluLeuProTrpGlu 391
```

RESULT 37
B97403
methionine adenosyltransferase (EC 2.5.1.6) - Agrobacterium tumefaciens (strain C58, Cer
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: B97403
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; PMID:11743194
A;Accession: B97403
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-420 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK86179.1; PID:g15155274; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C_632
A;Map position: circular chromosome
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	2.44	Length:	420
Score:	61.00	Matches:	14
Percent Similarity:	63.33%	Conservative:	5
Best Local Similarity:	46.67%	Mismatches:	5
Query Match:	17.48%	Indels:	6
DB:	2	Gaps:	2

US-09-198-779B-1 (1-235) x B97403 (1-420)

```
Qy    163 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGAC---------GACGCCGACTTC 213
          :::   ||||||::::::|||||||||||||||||||           |||      |||
Db    384 TyrAlaLysThrSerSerTyrGlyHisPheGlyArgLysAlaGlyArgAspGlySerPhe 403

Qy    214 ACCTGCGAG---------GTGGTCAAGCCC 234
          :::   |||         :::||||||||||
Db    404 SerTrpGluLysLeuAspLeuValLysPro 413
```

RESULT 38
AB2621
S-adenosylmethionine synthetase metK [imported] - Agrobacterium tumefaciens (strain C
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C;Accession: AB2621
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AB2621
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-420 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL41384.1; PID:g17738701; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: metK
A;Map position: circular chromosome
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	2.44	Length:	420
Score:	61.00	Matches:	14
Percent Similarity:	63.33%	Conservative:	5
Best Local Similarity:	46.67%	Mismatches:	5
Query Match:	17.48%	Indels:	6
DB:	2	Gaps:	2

US-09-198-779B-1 (1-235) x AB2621 (1-420)

```
Qy    163 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGAC---------GACGCCGACTTC 213
          :::   ||||||::::::|||||||||||||||||||           |||      |||
Db    384 TyrAlaLysThrSerSerTyrGlyHisPheGlyArgLysAlaGlyArgAspGlySerPhe 403

Qy    214 ACCTGCGAG---------GTGGTCAAGCCC 234
          :::   |||         :::||||||||||
Db    404 SerTrpGluLysLeuAspLeuValLysPro 413
```

RESULT 39
AC2211
heme transport protein alr3242 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp.

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AC2211
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC2211
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-877 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74941.1; PID:g17132337; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr3242

Alignment Scores:

Pred. No.:	2.53	Length:	877
Score:	61.00	Matches:	13
Percent Similarity:	55.56%	Conservative:	7
Best Local Similarity:	36.11%	Mismatches:	16
Query Match:	17.48%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1 (1-235) x AC2211 (1-877)

```
Qy      12 AGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGT 71
           |||||||||   |||   |||       ::::::      |||          :::
Db     412 SerLeuGlyTyrGlnTyrAspAsnProAsnSerLysSerTrpLeuGlnPheValArgAla 431

Qy      72 TCGTTGTGTTATTAATGTTGTATAATTGAGCAGGACACAACACGTACG 119
           :::|||   |||         |||||||||:::|||:::   |||:::
Db     432 AsnLeuTyrTyrGlnAsnAlaIleIleGluGluAspSerAsnArgSer 447
```

RESULT 40
S74736
methionine adenosyltransferase (EC 2.5.1.6) - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein sll0927; S-adenosylmethionine synthetase
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S74736
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74736
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-409 <KAN>
A;Cross-references: EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAA16887.1; PID:g165196
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: metX
A;Start codon: GTG
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	2.9	Length:	409
Score:	60.50	Matches:	13
Percent Similarity:	68.18%	Conservative:	2
Best Local Similarity:	59.09%	Mismatches:	6
Query Match:	17.34%	Indels:	1
DB:	2	Gaps:	1

US-09-198-779B-1 (1-235) x S74736 (1-409)

```
Qy     160 AGGTTCATCAAG---ACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACC 216
           ||||||   :::     ||||||||||||||||||||||||:::|||   |||
Db     367 ArgPheTyrGlnAspValAlaAlaTyrGlyHisPheGlyArgAsnAspLeuAspLeuPro 386

Qy     217 TGCGAG 222
               |||
Db     387 TrpGlu 388
```

RESULT 41
E82319
S-adenosylmethionine synthase VC0472 [imported] - Vibrio cholerae (strain N16961 sero
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: E82319
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: E82319
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-385 <HEI>
A;Cross-references: GB:AE004133; GB:AE003852; NID:g9654889; PIDN:AAF93645.1; GSPDB:GN
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0472
A;Map position: 1
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	3.45	Length:	385
Score:	60.00	Matches:	10
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	83.33%	Mismatches:	0
Query Match:	17.19%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1 (1-235) x E82319 (1-385)

```
Qy     169 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGAC 204
           ||||||||||||||||||||||||||||||::::::
Db     355 LysThrAlaAlaTyrGlyHisPheGlyArgGluGlu 366
```

RESULT 42
B84381
acylaminoacyl-peptidase [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: B84381
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: B84381
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-674 <STO>
A;Cross-references: GB:AE004437; NID:g10581715; PIDN:AAG20414.1; GSPDB:GN00138
C;Genetics:
A;Gene: yuxL

Alignment Scores:

Pred. No.:	3.54	Length:	674
Score:	60.00	Matches:	25
Percent Similarity:	31.03%	Conservative:	2
Best Local Similarity:	28.74%	Mismatches:	28
Query Match:	17.34%	Indels:	32
DB:	2	Gaps:	3

US-09-198-779B-1 (1-235) x B84381 (1-674)

```
Qy    228 GACCACCTCGCAGGTGAAGTCGGCGTCGTCACGGCCAAAGTGGCCGTATGCGGC------ 175
          |||      ||||||   |||      |||||||||   ||||||   ||||||
Db    183 AspLeuAlaAlaGlyArgValAspArgValThrAlaGlyValAlaGluCysGlyGlyPro 202

Qy    174 ----------------------------------------GGTCTTGAT--------- 166
                                                  |||||||||
Db    203 AlaTrpGlyAspAspGlyThrLeuTyrTyrProIleArgArgGlyLeuAspAlaAspAsp 222

Qy    165 ------GAACCTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAACGTACGTG 112
                 |||                                          |||   |||
Db    223 ArgLeuGluTrpAlaIleGluAlaAlaThrProAlaAspSerAlaAspSerThrValVal 242

Qy    111 TTGTGTCCTGCTCAATTATACAACATTAATAACACAACGAACAATGGATCAGGACCGTCC 52
                                       ||||||      |||   |||||||:::
Db    243 ---------------------------------ThrThrValGluGlyMetGlyProThr 251

Qy     51 ATTTATCAGCATGGGCAGCGT 31
          :::      ||||||   |||
Db    252 LeuAlaValHisGlySerArg 258
```

RESULT 43
A71281
probable S-adenosylmethionine synthetase (metK) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 18-Jun-1999
C;Accession: A71281
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: A71281
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-396 <COL>
A;Cross-references: GB:AE001250; GB:AE000520; NID:g3323096; PIDN:AAC65758.1; PID:g332310
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0794
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	4.89	Length:	396
Score:	59.00	Matches:	13
Percent Similarity:	54.55%	Conservative:	5
Best Local Similarity:	39.39%	Mismatches:	7
Query Match:	16.91%	Indels:	8
DB:	2	Gaps:	2

US-09-198-779B-1 (1-235) x A71281 (1-396)

```
Qy    160 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGAC--------------- 204
          |||:::      ||||||   |||||||||||||||||||:::
Db    355 ArgTyrArgSerThrAlaValTyrGlyHisPheGlyArgGluGlnPheProTrpGluArg 374

Qy    205 GCCGACTTCACCTGCGAGGTG---------GTCAAGCCC 234
             |||      |||::::::         |||:::|||
Db    375 ThrAspCysValCysAspLeuGlnArgAlaValArgPro 387
```

RESULT 44
A47151
methionine adenosyltransferase (EC 2.5.1.6) - mouse
N;Alternate names: S-adenosylmethionine synthetase
C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-May-2000
C;Accession: A47151
R;Sakata, S.F.; Shelly, L.L.; Ruppert, S.; Schutz, G.; Chou, J.Y.
J. Biol. Chem. 268, 13978-13986, 1993
A;Title: Cloning and expression of murine S-adenosylmethionine synthetase.
A;Reference number: A47151; MUID:93300783; PMID:8314764
A;Accession: A47151
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-396 <SAK>
A;Experimental source: liver
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:134412, NCBIP:134413)
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	4.89	Length:	396
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US-09-198-779B-1 (1-235) x A47151 (1-396)

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RESULT 45
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methionine adenosyltransferase (EC 2.5.1.6) - rat
N;Alternate names: S-adenosylmethionine synthetase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 05-May-2000
C;Accession: S06114; S18256; S18257
R;Horikawa, S.; Ishikawa, M.; Ozasa, H.; Tsukada, K.
Eur. J. Biochem. 184, 497-501, 1989
A;Title: Isolation of a cDNA encoding the rat liver S-adenosylmethionine synthetase.
A;Reference number: S06114; MUID:90032633; PMID:2806235
A;Accession: S06114
A;Molecule type: mRNA
A;Residues: 1-397 <HOR>
A;Cross-references: EMBL:X15734; NID:g57183; PIDN:CAA33754.1; PID:g57184
R;Mato, J.M.
submitted to the EMBL Data Library, July 1991
A;Reference number: S18256
A;Accession: S18256
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-397 <MAT>
A;Cross-references: EMBL:X60822
R;Alvarez, L.; Asuncion, M.; Corrales, F.; Pajares, M.A.; Mato, J.M.
FEBS Lett. 290, 142-146, 1991
A;Title: Analysis of the 5' non-coding region of rat liver S-adenosylmethionine synth
A;Reference number: S18257; MUID:92008649; PMID:1915866
A;Accession: S18257
A;Status: translation not shown
A;Molecule type: mRNA
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C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	4.89	Length:	397
Score:	59.00	Matches:	13
Percent Similarity:	71.43%	Conservative:	2
Best Local Similarity:	61.90%	Mismatches:	4
Query Match:	16.91%	Indels:	2
DB:	2	Gaps:	1

US-09-198-779B-1 (1-235) x S06114 (1-397)

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Qy    169 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTC 228
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```
          ||||||||||   ||||||||||||||||||      :::::|||      ||||||
Db     375 LysThrAlaCysTyrGlyHisPheGlyArg------SerGluPheProTrpGluValPro 392

Qy     229 AAG 231
           |||
Db     393 Lys 393
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Search completed: April 23, 2003, 12:07:53
Job time : 24.5833 secs

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: April 23, 2003, 12:06:52 ; Search time 55.9444 Seconds
(without alignments)
3059.318 Million cell updates/sec

Title: US-09-198-779B-1_COPY_160_235
Perfect score: 76
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	74.4	97.9	1674	21	AAC47744	Zea mays DNA fragm
2	64.8	85.3	1380	20	AAX07185	Wheat S-adenosylme
3	61.6	81.1	1182	19	AAT99143	S-adenosylmethioni
4	60	78.9	1182	19	AAT99141	S-adenosylmethioni
5	58.4	76.8	1182	19	AAT99142	S-adenosylmethioni
6	53.6	70.5	399	20	AAX81128	S-adenosyl methion
7	52	68.4	1485	20	AAX07184	Soybean S-adenosyl
8	52	68.4	1518	21	AAA51037	Soybean S-adenosyl
9	51	67.1	1582	20	AAX07183	Corn S-adenosylmet
10	50.4	66.3	635	21	AAC44219	Arabidopsis thalia
11	50.4	66.3	1508	21	AAC33986	Arabidopsis thalia
12	50.4	66.3	1521	21	AAC45478	Arabidopsis thalia
13	50.4	66.3	1529	21	AAC33535	Arabidopsis thalia
14	48.8	64.2	1653	21	AAC45944	Arabidopsis thalia
15	48.8	64.2	1654	21	AAC35348	Arabidopsis thalia
16	45.6	60.0	1636	22	AAD02296	Nicotiana tabacum
17	42.4	55.8	1393	21	AAC46421	Arabidopsis thalia
18	42.4	55.8	1395	21	AAC33674	Arabidopsis thalia
19	38.2	50.3	4848	24	AAD22684	Streptomyces fradi
20	38.2	50.3	4848	24	AAD22686	Streptomyces fradi
c 21	37.6	49.5	1693	21	AAA75637	Nucleotide sequenc
c 22	37.6	49.5	1693	21	AAZ56005	Contig 004 from co
23	37.4	49.2	297	24	ABL72111	Corn tassel-derive
24	37.4	49.2	1208	15	AAQ64204	snaC gene encoding
25	37.4	49.2	5392	15	AAQ64201	Sequence comprisin
26	34.4	45.3	4403765	22	AAI99683	Mycobacterium tube
27	34.4	45.3	4411529	22	AAI99682	Mycobacterium tube
28	32.8	43.2	56485	21	AAA81476	N. meningitidis pa
c 29	32.8	43.2	349980	21	AAF21612	Neisseria meningit
c 30	32.8	43.2	837096	21	AAA81489	N. meningitidis pa
c 31	30.6	40.3	606	23	AAS51580	Pseudomonas aerugi
32	28.6	37.6	657	21	AAF12426	Aspergillus oryzae
33	27.8	36.6	383	21	AAF08609	Fusarium venenatum
34	27.8	36.6	2284	24	ABK13571	Ryegrass 4-coumara
35	27.8	36.6	3600	17	AAT13227	Thermostable enzym
36	27.8	36.6	7584	20	AAX19362	Rhodococcus corall
37	27.8	36.6	7600	21	AAA51878	Rhodococcus sp. OH
38	27.6	36.3	1957	22	AAD07974	Rice cysteinyl-tRN
39	27.6	36.3	2907	24	ABQ90584	M. capsulatus gene
40	27.4	36.1	1791	20	AAZ25727	Stachybotrys chart
41	27.4	36.1	1791	20	AAZ27601	Stachybotrys pheno
42	27.4	36.1	1791	21	AAA50019	Stachybotrys chart
43	27.4	36.1	1791	21	AAA51314	Stachybotrys chart
44	27.4	36.1	1791	24	AAL47584	S chartarum phenol
45	27.4	36.1	7248	24	ABA92911	Stachybotrys chart
46	27.2	35.8	566	21	AAF08527	Fusarium venenatum
47	27.2	35.8	1104	23	ABL02251	Drosophila melanog
48	27.2	35.8	3178	23	ABL02250	Drosophila melanog
49	27	35.5	5676	19	AAV21186	Amycolatopsis medi
50	27	35.5	53789	19	AAV21187	Amycolatopsis medi

ALIGNMENTS

RESULT 1
AAC47744
ID AAC47744 standard; DNA; 1674 BP.
XX
AC AAC47744;
XX
DT 18-OCT-2000 (first entry)
XX
DE Zea mays DNA fragment SEQ ID NO: 54954.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic;
KW pathway; promoter; termination sequence; corn; ss.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR   29-OCT-1999;   99US-0162142.

  Query Match             97.9%;  Score 74.4;  DB 21;  Length 1674;
  Best Local Similarity   98.7%;  Pred. No. 5.5e-14;
  Matches   75;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
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Db   1188 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGG 1247

Qy     61 GAGGTGGTCAAGCCCC 76
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Db   1248 GAGGTGGTCAAGCCCC 1263


RESULT 2
AAX07185
ID   AAX07185 standard; cDNA; 1380 BP.
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AC   AAX07185;
XX
DT   21-MAY-1999  (first entry)
XX
DE   Wheat S-adenosylmethionine synthetase cDNA contig.
XX
KW   S-adenosylmethionine synthetase; wheat; amino acid; lysine;
KW   threonine; methionine; cysteine; isoleucine; transgenic plant;
KW   crop improvement; food; feedstuff; ss.
XX
OS   Triticum aestivum.
XX
FH   Key             Location/Qualifiers
FT   CDS             73..1257
FT                   /*tag=  a
XX
PN   WO9855601-A2.
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PD   10-DEC-1998.
XX
PF   05-JUN-1998;   98WO-US11692.
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PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
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PI   Abell LM,  Allen SM,  Falco SC,  Hitz WD,  Kinney AJ;
PI   Rafalski JA,  Thorpe CJ;
XX
DR   WPI; 1999-070263/06.
DR   P-PSDB; AAW97744.
XX
PT   New plant amino acid biosynthetic enzymes, DNA and chimeric genes -
PT   encode: dihydropicolinate reductase; diaminopimelate epimerase;
PT   threonine synthase; threonine deaminase; S-adenosylmethionine
PT   synthetase
XX
PS   Claim 47; Page 69-70; 98pp; English.
XX
CC   This is the nucleotide sequence of a cDNA contig that codes for
CC   a full-length wheat S-adenosylmethionine synthetase (see AAW97744).
CC   The contig was assembled from clones isolated from wheat kernel,
CC   leaf, seedling and root cDNA libraries and identified by comparison
CC   to public sequence databases using BLAST algorithms.  It shows
CC   sequence similarity to the barley enzyme.  The invention relates to
CC   new isolated nucleic acid fragments (see AAX07168-85) encoding plant
CC   enzymes (see AAW97727-44) that catalyse steps in the biosynthesis of
CC   lysine, threonine, methionine, cysteine and isoleucine from
CC   aspartate, the enzyme being selected from dihydropicolinate reductase,
CC   diaminopimelate epimerase, threonine synthase, threonine deaminase
CC   or S-adenosylmethionine synthetase.  The invention also relates to
CC   the construction of a chimeric gene encoding all or a portion of
CC   the biqsynthetic pathway enzyme, in sense or antisense orientation,
CC   where expression of the chimeric gene results in production of
CC   altered levels of the enzyme in a transformed host cell.
CC   Overexpression or reduction of expression of genes encoding the
CC   amino acid biosynthetic pathway enzymes in crop plants such as
CC   corn, soybean and wheat can be used to alter levels of the amino
CC   acids in human food and animal feed.  Transformed host cells can
CC   also be used to identify compounds that inhibit one of the enzymes.
XX
SQ   Sequence 1380 BP; 299 A; 430 C; 379 G; 267 T; 5 other;

  Query Match             85.3%;  Score 64.8;  DB 20;  Length 1380;
  Best Local Similarity   90.8%;  Pred. No. 5.2e-11;
  Matches   69;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
          |||||||||||||||| || ||||| |||||||||||||| || ||||||||||||||
Db   1156 AGGTTCATCAAGACCGCTGCTTACGGTCACTTTGGCCGTGATGATGCCGACTTCACCTGG 1215

Qy     61 GAGGTGGTCAAGCCCC 76
          |||||||| |||||||
Db   1216 GAGGTGGTGAAGCCCC 1231


RESULT 3
AAT99143
ID   AAT99143 standard; cDNA to mRNA; 1182 BP.
XX
AC   AAT99143;
XX
DT   26-MAR-1998  (first entry)
XX
DE   S-adenosylmethionine synthase 3 gene.
XX
KW   S-adenosylmethionine synthase 3 gene; barley; alkali resistant plant;
KW   sam3; ss.
XX
OS   Hordeum vulgare.
XX
PN   JP09313186-A.
XX
PD   09-DEC-1997.
XX
PF   28-MAY-1996;   96JP-0133406.
XX
PR   28-MAY-1996;   96JP-0133406.
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XX
PA   (NIOC ) NIPPON OIL CO LTD.
XX
DR   WPI; 1998-080077/08.
DR   P-PSDB; AAW34542.
XX
PT   S-adenosyl-methionine synthase gene - useful in producing plants
PT   resistant to alkaline soil
XX
PS   Claim 6; Page 10-11; 13pp; Japanese.
XX
CC   This sequence represents the S-adenosylmethionine synthase 3 (sam3)
CC   gene. This DNA sequence may be used in a vector to produce plants which
CC   are resistant to alkaline soil.
XX
SQ   Sequence 1182 BP; 253 A; 368 C; 331 G; 230 T; 0 other;

  Query Match            81.1%;  Score 61.6;  DB 19;  Length 1182;
  Best Local Similarity  88.2%;  Pred. No. 5.1e-10;
  Matches   67;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy      1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
          ||||||||||||||| || || || || |||||||||| ||||| ||||||||||||||
Db   1084 AGGTTCATCAAGACAGCTGCTTATGGTCACTTTGGCCGCGACGATGCCGACTTCACCTGG 1143

Qy     61 GAGGTGGTCAAGCCCC 76
          |||||||| |||||||
Db   1144 GAGGTGGTGAAGCCCC 1159


RESULT 4
AAT99141
ID   AAT99141 standard; cDNA to mRNA; 1182 BP.
XX
AC   AAT99141;
XX
DT   26-MAR-1998  (first entry)
XX
DE   S-adenosylmethionine synthase 1 gene.
XX
KW   S-adenosylmethionine synthase 1 gene; barley; alkali resistant plant;
KW   sam1; ss.
XX
OS   Hordeum vulgare.
XX
PN   JP09313186-A.
XX
PD   09-DEC-1997.
XX
PF   28-MAY-1996;   96JP-0133406.
XX
PR   28-MAY-1996;   96JP-0133406.
XX
PA   (NIOC ) NIPPON OIL CO LTD.
XX
DR   WPI; 1998-080077/08.
DR   P-PSDB; AAW34540.
XX
PT   S-adenosyl-methionine synthase gene - useful in producing plants
PT   resistant to alkaline soil
XX
PS   Claim 4; Page 8-9; 13pp; Japanese.
XX
CC   This sequence represents the S-adenosylmethionine synthase 1 (sam1)
CC   gene. This DNA sequence may be used in a vector to produce plants which
CC   are resistant to alkaline soil.
XX
SQ   Sequence 1182 BP; 253 A; 372 C; 324 G; 233 T; 0 other;

  Query Match            78.9%;  Score 60;  DB 19;  Length 1182;
  Best Local Similarity  86.8%;  Pred. No. 1.6e-09;
  Matches   66;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy      1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
          |||||||||||||| || || ||||| |||||||||| || || || ||||||||||
Db   1084 AGGTTCATCAAGACAGCTGCTTACGGTCACTTTGGCCGCGATGATGCTGACTTCACCTGG 1143

Qy     61 GAGGTGGTCAAGCCCC 76
          |||||||| |||||||
Db   1144 GAGGTGGTGAAGCCCC 1159


RESULT 5
AAT99142
ID   AAT99142 standard; cDNA to mRNA; 1182 BP.
XX
AC   AAT99142;
XX
DT   26-MAR-1998  (first entry)
XX
DE   S-adenosylmethionine synthase 2 gene.
XX
KW   S-adenosylmethionine synthase 2 gene; barley; alkali resistant plant;
KW   sam2; ss.
XX
OS   Hordeum vulgare.
XX
PN   JP09313186-A.
XX
PD   09-DEC-1997.
XX
PF   28-MAY-1996;   96JP-0133406.
XX
PR   28-MAY-1996;   96JP-0133406.
XX
PA   (NIOC ) NIPPON OIL CO LTD.
XX
DR   WPI; 1998-080077/08.
DR   P-PSDB; AAW34541.
XX
PT   S-adenosyl-methionine synthase gene - useful in producing plants
PT   resistant to alkaline soil
XX
PS   Claim 5; Page 9-10; 13pp; Japanese.
XX
CC   This sequence represents the S-adenosylmethionine synthase 2 (sam2)
CC   gene. This DNA sequence may be used in a vector to produce plants which
CC   are resistant to alkaline soil.
XX
SQ   Sequence 1182 BP; 261 A; 368 C; 324 G; 229 T; 0 other;

  Query Match            76.8%;  Score 58.4;  DB 19;  Length 1182;
  Best Local Similarity  85.5%;  Pred. No. 5e-09;
  Matches   65;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy      1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
          |||||||||||||| || || ||||| ||||| ||||| || || || ||||||||||
Db   1084 AGGTTCATCAAGACAGCTGCTTACGGTCACTTCGGCCGCGATGATGCTGACTTCACCTGG 1143

Qy     61 GAGGTGGTCAAGCCCC 76
          |||||||| |||||||
Db   1144 GAGGTGGTGAAGCCCC 1159


RESULT 6
AAX81128
ID   AAX81128 standard; cDNA; 399 BP.
XX
AC   AAX81128;
XX
DT   06-SEP-1999  (first entry)
XX
DE   S-adenosyl methionine (SAM) partial cDNA sequence.
XX
KW   Senescence-associated receptor-like protein kinase; sark; sam gene; sag;
KW   senescence-associated gene; plant senescence; promoter; pharmaceutical;
```

KW plant maturation; S-adenosyl methionine; flower; fruit development; ss.
XX
OS Phaseolus vulgaris.
XX
PN WO9929159-A1.
XX
PD 17-JUN-1999.
XX
PF 08-DEC-1998; 98WO-US25799.
XX
PR 08-DEC-1997; 97US-0067898.
XX
PA (VITA-) VITALITY BIOTECHNOLOGIES INC.
XX
PI Gepstein S, Hajuoje T, Rosner A;
XX
DR WPI; 1999-404873/34.
DR P-PSDB; AAY21978.
XX
PT DNA encoding senescence-associated genes for a senescence
PT receptor-like protein kinase
XX
PS Claim 18; Fig 4; 70pp; English.
XX
CC The invention relates to a senescence-associated receptor-like protein
CC kinase (sark) gene. The sark gene is a senescence-associated gene (sag)
CC and is expressed early in the plant senescence process. The sark gene
CC promoter is useful for driving expression of foreign genes having a
CC desired product, such as a pharmaceutical, during the process of plant
CC maturation. The sark gene promoter can be used to drive expression of
CC resistance genes against pathogens or pests during senescence when the
CC plant is particularly susceptible to infection or infestation. The sark
CC gene promoter may also be used to drive expression of a gene encoding an
CC inhibitor of senescence. Plant senescence may be inhibited by use of
CC antisense sark constructs. Over expression of the sag genes, using the
CC sark or sam (S-adenosyl methionine) gene promoters is useful for
CC induction of early senescence. This is useful to obtain flower or fruit
CC development prior to specific pest onset, prior to undesirable cross-
CC fertilization from related crops, at a specific time during storage or
CC retail, or to avoid development of plant structures that are not of
CC agronomic importance. The present sequence represents a partial cDNA
CC clone of S-adenosyl methionine (SAM).
XX
SQ Sequence 399 BP; 108 A; 80 C; 82 G; 129 T; 0 other;

Query Match 70.5%; Score 53.6; DB 20; Length 399;
Best Local Similarity 81.6%; Pred. No. 1.4e-07;
Matches 62; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

```
Qy       1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
           |||||| | ||||| || ||||| || ||||| ||| | || ||||| |||||||| ||
Db     102 AGGTTCTTGAAGACTGCTGCATATGGACACTTCGGCAGAGAGGACGCTGACTTCACATGG 161

Qy      61 GAGGTGGTCAAGCCCC 76
           || ||||||||||||||
Db     162 GAAGTGGTCAAGCCCC 177
```

RESULT 7
AAX07184
ID AAX07184 standard; cDNA; 1485 BP.
XX
AC AAX07184;
XX
DT 21-MAY-1999 (first entry)
XX
DE Soybean S-adenosylmethionine synthetase cDNA clone s2.12b06.
XX
KW S-adenosylmethionine synthetase; soybean; amino acid; lysine;
KW threonine; methionine; cysteine; isoleucine; transgenic plant;
KW crop improvement; food; feedstuff; ss.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FT CDS 74..1252
FT /*tag= a
XX
PN WO9855601-A2.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US11692.
XX
PR 12-JUN-1997; 97US-0049443.
PR 06-JUN-1997; 97US-0048771.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Abell LM, Allen SM, Falco SC, Hitz WD, Kinney AJ;
PI Rafalski JA, Thorpe CJ;
XX
DR WPI; 1999-070263/06.
DR P-PSDB; AAW97743.
XX
PT New plant amino acid biosynthetic enzymes, DNA and chimeric genes -
PT encode: dihydropicolinate reductase; diaminopimelate epimerase;
PT threonine synthase; threonine deaminase; S-adenosylmethionine
PT synthetase
XX
PS Claim 44; Page 66-67; 98pp; English.
XX
CC This is the nucleotide sequence of cDNA clone s2.12b06, which
CC codes for a full-length soybean S-adenosylmethionine synthetase
CC (see AAW97743). The clone was isolated from a soybean seed cDNA
CC library and identified by comparison to public sequence databases
CC using BLAST algorithms. It shows sequence similarity to the
CC tomato enzyme. The invention relates to new isolated nucleic
CC acid fragments (see AAX07168-85) encoding plant enzymes (see
CC AAW97727-44) that catalyse steps in the biosynthesis of lysine,
CC threonine, methionine, cysteine and isoleucine from aspartate, the
CC enzyme being selected from dihydropicolinate reductase,
CC diaminopimelate epimerase, threonine synthase, threonine deaminase
CC or S-adenosylmethionine synthetase. The invention also relates to
CC the construction of a chimeric gene encoding all or a portion of
CC the biosynthetic pathway enzyme, in sense or antisense orientation,
CC where expression of the chimeric gene results in production of
CC altered levels of the enzyme in a transformed host cell.
CC Overexpression or reduction of expression of genes encoding the
CC amino acid biosynthetic pathway enzymes in crop plants such as
CC corn, soybean and wheat can be used to alter levels of the amino
CC acids in human food and animal feed. Transformed host cells can
CC also be used to identify compounds that inhibit one of the enzymes.
XX
SQ Sequence 1485 BP; 366 A; 373 C; 357 G; 389 T; 0 other;

Query Match 68.4%; Score 52; DB 20; Length 1485;
Best Local Similarity 80.3%; Pred. No. 5.1e-07;
Matches 61; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

```
Qy       1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
           |||||| | ||||| || ||||| || ||||| ||| | || ||| | ||||||||  ||
Db    1157 AGGTTCTTGAAGACTGCTGCATATGGACACTTCGGCAGAGAGGACCCTGACTTCACATGG 1216

Qy      61 GAGGTGGTCAAGCCCC 76
           || ||||||||||||||
Db    1217 GAAGTGGTCAAGCCCC 1232
```

RESULT 8
AAA51037
ID AAA51037 standard; cDNA; 1518 BP.
XX
AC AAA51037;
XX
DT 09-OCT-2000 (first entry)

```
XX
DE   Soybean S-adenosyl-L-methionine synthetase cDNA.
XX
KW   S-adenosyl-L-methionine synthetase; SAMS; probe; promoter; embryo;
KW   constitutive; tissue-specific; development-specific;
KW   herbicide resistance; pathogen resistance; ss.
XX
OS   Glycine max.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..73
FT                   /*tag= a
FT   CDS             74..1252
FT                   /*tag= b
FT                   /product= S-adenosyl-L-methionine_Synthetase
XX
PN   WO200037662-A2.
XX
PD   29-JUN-2000.
XX
PF   17-DEC-1999;   99WO-US30180.
XX
PR   21-DEC-1998;   98US-0113045.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Falco SC,  Li Z;
XX
DR   WPI; 2000-442682/38.
XX
PT   S-adenosyl-L-methionine synthetase promoter for expressing target
PT   heterologous herbicide-resistance or pathogen-resistance nucleic acid
PT   fragments in plants, especially soybean
XX
PS   Example 2; Page 39; 50pp; English.
XX
CC   This is the soybean full-length S-adenosyl-L-methionine synthetase (SAMS)
CC   cDNA, which was used to generate a probe to isolate a SAMS promoter. The
CC   SAMS promoter is active in seedlings and callus and over-expression of a
CC   gene in embryo stage can be achieved at an early developing stage using
CC   the SAMS promoter. The SAMS promoter may be used as an alternative to
CC   cauliflower mosaic virus 35S promoter to drive expression of selectable
CC   marker genes. Plant cells transformed with the SAMS constitutive promoter
CC   are useful for increasing or decreasing the expression of heterologous
CC   nucleic acid fragments in a plant, preferably corn, rice, wheat, barley,
CC   palm, Arabidopsis, soybean, oil seed Brassica, peanut, sunflower,
CC   safflower, cotton, tobacco, tomato, potato or cocoa. Target heterologous
CC   nucleic acid fragments include herbicide or pathogen resistance
CC   nucleic acid fragments.
XX
SQ   Sequence 1518 BP; 399 A; 373 C; 357 G; 389 T; 0 other;

  Query Match             68.4%;  Score 52;  DB 21;  Length 1518;
  Best Local Similarity   80.3%;  Pred. No. 5.1e-07;
  Matches   61;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy       1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
           |||||| | ||||| || ||||| || ||||| ||| | || ||| | ||||||||  ||
Db    1157 AGGTTCTTGAAGACTGCTGCATATGGACACTTCGGCAGAGAGGACCCTGACTTCACATGG 1216

Qy      61 GAGGTGGTCAAGCCCC 76
           || ||||||||||||||
Db    1217 GAAGTGGTCAAGCCCC 1232


RESULT 9
AAX07183
ID   AAX07183 standard; cDNA; 1582 BP.
XX
AC   AAX07183;
XX
DT   21-MAY-1999  (first entry)
XX
DE   Corn S-adenosylmethionine synthetase cDNA clone cc3.mn0002.d2.
XX
KW   S-adenosylmethionine synthetase; corn; maize; amino acid; lysine;
KW   threonine; methionine; cysteine; isoleucine; transgenic plant;
KW   crop improvement; food; feedstuff; ss.
XX
OS   Zea mays.
XX
FH   Key             Location/Qualifiers
FT   CDS             140..1330
FT                   /*tag= a
XX
PN   WO9855601-A2.
XX
PD   10-DEC-1998.
XX
PF   05-JUN-1998;   98WO-US11692.
XX
PR   12-JUN-1997;   97US-0049443.
PR   06-JUN-1997;   97US-0048771.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Abell LM,  Allen SM,  Falco SC,  Hitz WD,  Kinney AJ;
PI   Rafalski JA,  Thorpe CJ;
XX
DR   WPI; 1999-070263/06.
DR   P-PSDB; AAW97742.
XX
PT   New plant amino acid biosynthetic enzymes, DNA and chimeric genes -
PT   encode: dihydropicolinate reductase; diaminopimelate epimerase;
PT   threonine synthase; threonine deaminase; S-adenosylmethionine
PT   synthetase
XX
PS   Claim 41; Page 62-63; 98pp; English.
XX
CC   This is the nucleotide sequence of cDNA clone cc3.mn0002.d2, which
CC   codes for a full-length corn S-adenosylmethionine synthetase
CC   (see AAW97742).  The clone was isolated from a corn callus cDNA
CC   library and identified by comparison to public sequence databases
CC   using BLAST algorithms.  It shows sequence similarity to the
CC   Oryza sativa enzyme.  The invention relates to new isolated
CC   nucleic acid fragments (see AAX07168-85) encoding plant enzymes (see
CC   AAW97727-44) that catalyse steps in the biosynthesis of lysine,
CC   threonine, methionine, cysteine and isoleucine from aspartate, the
CC   enzyme being selected from dihydropicolinate reductase,
CC   diaminopimelate epimerase, threonine synthase, threonine deaminase
CC   or S-adenosylmethionine synthetase.  The invention also relates to
CC   the construction of a chimeric gene encoding all or a portion of
CC   the biosynthetic pathway enzyme, in sense or antisense orientation,
CC   where expression of the chimeric gene results in production of
CC   altered levels of the enzyme in a transformed host cell.
CC   Overexpression or reduction of expression of genes encoding the
CC   amino acid biosynthetic pathway enzymes in crop plants such as
CC   corn, soybean and wheat can be used to alter levels of the amino
CC   acids in human food and animal feed.  Transformed host cells can
CC   also be used to identify compounds that inhibit one of the enzymes.
XX
SQ   Sequence 1582 BP; 340 A; 474 C; 417 G; 351 T; 0 other;

  Query Match             67.1%;  Score 51;  DB 20;  Length 1582;
  Best Local Similarity   80.0%;  Pred. No. 1e-06;
  Matches   60;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy       2 GGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCG 61
           | | | ||||||| || || |||||||||||| ||  | |||||| | |||||||||||| |
Db    1230 GCTACCTCAAGACGGCAGCCTACGGCCACTTCGGAAGGGACGACCCTGACTTCACCTGGG 1289

Qy      62 AGGTGGTCAAGCCCC 76
           ||||||| ||||| |
Db    1290 AGGTGGTGAAGCCAC 1304
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```
RESULT 10
AAC44219
ID   AAC44219 standard; DNA; 635 BP.
XX
AC   AAC44219;
XX
DT   18-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana DNA fragment SEQ ID NO: 42062.
XX
KW   Hybridisation assay; genetic mapping; gene expression control;
KW   protein identification; signal transduction pathway;
KW   metabolic pathway; promoter; termination sequence; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;   99US-0121825.
PR   05-MAR-1999;   99US-0123180.
PR   09-MAR-1999;   99US-0123548.
PR   23-MAR-1999;   99US-0125788.
PR   25-MAR-1999;   99US-0126264.
PR   29-MAR-1999;   99US-0126785.
PR   01-APR-1999;   99US-0127462.
PR   06-APR-1999;   99US-0128234.
PR   08-APR-1999;   99US-0128714.
PR   16-APR-1999;   99US-0129845.
PR   19-APR-1999;   99US-0130077.
PR   21-APR-1999;   99US-0130449.
PR   23-APR-1999;   99US-0130510.
PR   23-APR-1999;   99US-0130891.
PR   28-APR-1999;   99US-0131449.
PR   30-APR-1999;   99US-0132048.
PR   30-APR-1999;   99US-0132407.
PR   04-MAY-1999;   99US-0132484.
PR   05-MAY-1999;   99US-0132485.
PR   06-MAY-1999;   99US-0132486.
PR   06-MAY-1999;   99US-0132487.
PR   07-MAY-1999;   99US-0132863.
PR   11-MAY-1999;   99US-0134256.
PR   14-MAY-1999;   99US-0134218.
PR   14-MAY-1999;   99US-0134219.
PR   14-MAY-1999;   99US-0134221.
PR   14-MAY-1999;   99US-0134370.
PR   18-MAY-1999;   99US-0134768.
PR   19-MAY-1999;   99US-0134941.
PR   20-MAY-1999;   99US-0135124.
PR   21-MAY-1999;   99US-0135353.
PR   24-MAY-1999;   99US-0135629.
PR   25-MAY-1999;   99US-0136021.
PR   27-MAY-1999;   99US-0136392.
PR   28-MAY-1999;   99US-0136782.
PR   01-JUN-1999;   99US-0137222.
PR   03-JUN-1999;   99US-0137528.
PR   04-JUN-1999;   99US-0137502.
PR   07-JUN-1999;   99US-0137724.
PR   08-JUN-1999;   99US-0138094.
PR   10-JUN-1999;   99US-0138540.
PR   10-JUN-1999;   99US-0138847.
PR   14-JUN-1999;   99US-0139119.
PR   16-JUN-1999;   99US-0139452.
PR   16-JUN-1999;   99US-0139453.
PR   17-JUN-1999;   99US-0139492.
PR   18-JUN-1999;   99US-0139454.
PR   18-JUN-1999;   99US-0139455.
PR   18-JUN-1999;   99US-0139456.
PR   18-JUN-1999;   99US-0139457.
PR   18-JUN-1999;   99US-0139458.
PR   18-JUN-1999;   99US-0139459.
PR   18-JUN-1999;   99US-0139460.
PR   18-JUN-1999;   99US-0139461.
PR   18-JUN-1999;   99US-0139462.
PR   18-JUN-1999;   99US-0139463.
PR   18-JUN-1999;   99US-0139750.
PR   18-JUN-1999;   99US-0139763.
PR   21-JUN-1999;   99US-0139817.
PR   22-JUN-1999;   99US-0139899.
PR   23-JUN-1999;   99US-0140353.
PR   23-JUN-1999;   99US-0140354.
PR   24-JUN-1999;   99US-0140695.
PR   28-JUN-1999;   99US-0140823.
PR   29-JUN-1999;   99US-0140991.
PR   30-JUN-1999;   99US-0141287.
PR   01-JUL-1999;   99US-0141842.
PR   01-JUL-1999;   99US-0142154.
PR   02-JUL-1999;   99US-0142055.
PR   06-JUL-1999;   99US-0142390.
PR   08-JUL-1999;   99US-0142803.
PR   09-JUL-1999;   99US-0142920.
PR   12-JUL-1999;   99US-0142977.
PR   13-JUL-1999;   99US-0143542.
PR   14-JUL-1999;   99US-0143624.
PR   15-JUL-1999;   99US-0144005.
PR   16-JUL-1999;   99US-0144085.
PR   16-JUL-1999;   99US-0144086.
PR   19-JUL-1999;   99US-0144325.
PR   19-JUL-1999;   99US-0144331.
PR   19-JUL-1999;   99US-0144332.
PR   19-JUL-1999;   99US-0144333.
PR   19-JUL-1999;   99US-0144334.
PR   19-JUL-1999;   99US-0144335.
PR   20-JUL-1999;   99US-0144352.
PR   20-JUL-1999;   99US-0144632.
PR   20-JUL-1999;   99US-0144884.
PR   21-JUL-1999;   99US-0144814.
PR   21-JUL-1999;   99US-0145086.
PR   21-JUL-1999;   99US-0145088.
PR   22-JUL-1999;   99US-0145085.
PR   22-JUL-1999;   99US-0145087.
PR   22-JUL-1999;   99US-0145089.
PR   22-JUL-1999;   99US-0145192.
PR   23-JUL-1999;   99US-0145145.
PR   23-JUL-1999;   99US-0145218.
PR   23-JUL-1999;   99US-0145224.
PR   26-JUL-1999;   99US-0145276.
PR   27-JUL-1999;   99US-0145913.
PR   27-JUL-1999;   99US-0145918.
PR   27-JUL-1999;   99US-0145919.
PR   28-JUL-1999;   99US-0145951.
PR   02-AUG-1999;   99US-0146386.
PR   02-AUG-1999;   99US-0146388.
PR   02-AUG-1999;   99US-0146389.
PR   03-AUG-1999;   99US-0147038.
PR   04-AUG-1999;   99US-0147204.
PR   04-AUG-1999;   99US-0147302.
PR   05-AUG-1999;   99US-0147192.
PR   05-AUG-1999;   99US-0147260.
PR   06-AUG-1999;   99US-0147303.
PR   06-AUG-1999;   99US-0147416.
PR   09-AUG-1999;   99US-0147493.
PR   09-AUG-1999;   99US-0147935.
PR   10-AUG-1999;   99US-0148171.
PR   11-AUG-1999;   99US-0148319.
PR   12-AUG-1999;   99US-0148341.
PR   13-AUG-1999;   99US-0148565.
PR   13-AUG-1999;   99US-0148684.
PR   16-AUG-1999;   99US-0149368.
PR   17-AUG-1999;   99US-0149175.
PR   18-AUG-1999;   99US-0149426.
PR   20-AUG-1999;   99US-0149722.
PR   20-AUG-1999;   99US-0149723.
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PR   20-AUG-1999;   99US-0149929.
PR   23-AUG-1999;   99US-0149902.
PR   23-AUG-1999;   99US-0149930.
PR   25-AUG-1999;   99US-0150566.
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KW   protein identification; signal transduction pathway;
KW   metabolic pathway; promoter; termination sequence; ss.
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Query Match 66.3%; Score 50.4; DB 21; Length 1508;
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DT 18-OCT-2000 (first entry)
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
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XX
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  Query Match          66.3%;  Score 50.4;  DB 21;  Length 1521;
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Db    1228 GAGGTAGTCAAGCCAC 1243


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AC   AAC33535;
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DT   17-OCT-2000  (first entry)
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DE   Arabidopsis thaliana DNA fragment SEQ ID NO: 3408.
XX
KW   Hybridisation assay; genetic mapping; gene expression control;
KW   protein identification; signal transduction pathway;
KW   metabolic pathway; promoter; termination sequence; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
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Query Match 66.3%; Score 50.4; DB 21; Length 1529;
Best Local Similarity 78.9%; Pred. No. 1.6e-06;
Matches 60; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Db   1210 AGGTTCTTGAAAACTGCGGCTTACGGACACTTTGGAAGAGACGACCCTGACTTCACCTGG 1269

Qy     61 GAGGTGGTCAAGCCCC 76
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Db   1270 GAAGTCGTCAAGCCAC 1285
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RESULT 14
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ID AAC45944 standard; DNA; 1653 BP.
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AC AAC45944;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 48340.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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Qy      61 GAGGTGGTCAAGCCCC 76
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RESULT 15
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XX
AC AAC35348;
XX
DT 17-OCT-2000 (first entry)
XX
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XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.

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PN EP1033405-A2.
XX
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PF 25-FEB-2000; 2000EP-0301439.
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PR 01-JUL-1999; 99US-0141842.
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PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 64.2%; Score 48.8; DB 21; Length 1654;
Best Local Similarity 77.6%; Pred. No. 5.1e-06;
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Qy      61 GAGGTGGTCAAGCCCC 76
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Db    1289 GAGGTTGTCAAGCCGC 1304
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RESULT 16
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ID AAD02296 standard; DNA; 1636 BP.
XX
AC AAD02296;
XX
DT 28-MAR-2001 (first entry)
XX
DE Nicotiana tabacum S-adenosylmethionine synthetase (SAMS) DNA.
XX
KW Tobacco; alkaloid; nicotine; transgenic plant; pharmaceutical protein;
KW herbicide resistance; S-adenosylmethionine synthetase; SAMS; ds.
XX
OS Nicotiana tabacum.
XX
FH Key Location/Qualifiers
FT CDS 96..1268
FT /*tag= a

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FT                   /product= "Nicotiana tabacum S-adenosylmethionine
FT                   synthetase (SAMS) protein"
XX
PN   WO200067558-A1.
XX
PD   16-NOV-2000.
XX
PF   05-MAY-2000; 2000WO-US12450.
XX
PR   06-MAY-1999;   99US-0132919.
XX
PA   (TIMK/) TIMKO M.
XX
PI   Timko M;
XX
DR   WPI; 2001-007279/01.
DR   P-PSDB; AAY72078.
XX
PT   New nucleic acid encoding alkaloid-synthesis enzymes in tobacco, useful
PT   e.g. for producing transgenic plants with altered nicotine content  -
XX
PS   Claim 1; Page 78-79; 103pp; English.
XX
CC   The invention relates to enzymes involved in alkaloid, specifically
CC   nicotine, synthesis in tobacco and nucleic acids encoding them. The
CC   nucleic acid of the invention can be used, in sense or antisense
CC   orientation, to produce transgenic tobacco plants with altered
CC   alkaloid content, and also for expression of exogenous proteins,
CC   e.g. pharmaceutical proteins or proteins implicated in resistance
CC   to herbicides. The protein of the invention can be used to
CC   identify modulators of enzymatic activity in plants.
CC   The present sequence is Nicotiana tabacum S-adenosylmethionine
CC   synthetase (SAMS) DNA. This enzyme is involved in the nicotine
CC   biosynthetic pathway.
XX
SQ   Sequence 1636 BP; 444 A; 365 C; 373 G; 454 T; 0 other;

  Query Match             60.0%;  Score 45.6;  DB 22;  Length 1636;
  Best Local Similarity   75.0%;  Pred. No. 5e-05;
  Matches   57;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

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           |||| |   ||||| || || || || |||||||||||||| ||| ||||||| | ||
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Qy      61 GAGGTGGTCAAGCCCC 76
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Db    1236 GAGACTGTCAAGGTCC 1251


RESULT 17
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XX
AC   AAC46421;
XX
DT   18-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana DNA fragment SEQ ID NO: 50076.
XX
KW   Hybridisation assay; genetic mapping; gene expression control;
KW   protein identification; signal transduction pathway;
KW   metabolic pathway; promoter; termination sequence; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
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PR   25-FEB-1999;   99US-0121825.
PR   05-MAR-1999;   99US-0123180.
PR   09-MAR-1999;   99US-0123548.
PR   23-MAR-1999;   99US-0125788.
PR   25-MAR-1999;   99US-0126264.
PR   29-MAR-1999;   99US-0126785.
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PR   08-APR-1999;   99US-0128714.
PR   16-APR-1999;   99US-0129845.
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PR   23-APR-1999;   99US-0130891.
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PR   30-JUN-1999;   99US-0141287.
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PR 28-OCT-1999; 99US-0161992.
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Query Match 55.8%; Score 42.4; DB 21; Length 1393;
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Matches 55; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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Qy      61 GAGGTGGTCAAGCCCC 76
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Db    1235 GAGGTCGTGAAGCCAC 1250
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RESULT 18
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ID AAC33674 standard; DNA; 1395 BP.
XX
AC AAC33674;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 3906.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
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PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.
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PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.

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PR   08-OCT-1999;   99US-0158232.
PR   12-OCT-1999;   99US-0158369.
PR   13-OCT-1999;   99US-0159293.
PR   13-OCT-1999;   99US-0159294.
PR   13-OCT-1999;   99US-0159295.
PR   14-OCT-1999;   99US-0159329.
PR   14-OCT-1999;   99US-0159330.
PR   14-OCT-1999;   99US-0159331.
PR   14-OCT-1999;   99US-0159637.
PR   14-OCT-1999;   99US-0159638.
PR   18-OCT-1999;   99US-0159584.
PR   21-OCT-1999;   99US-0160741.
PR   21-OCT-1999;   99US-0160767.
PR   21-OCT-1999;   99US-0160768.
PR   21-OCT-1999;   99US-0160770.
PR   21-OCT-1999;   99US-0160814.
PR   21-OCT-1999;   99US-0160815.
PR   22-OCT-1999;   99US-0160980.
PR   22-OCT-1999;   99US-0160981.
PR   22-OCT-1999;   99US-0160989.
PR   25-OCT-1999;   99US-0161404.
PR   25-OCT-1999;   99US-0161405.
PR   25-OCT-1999;   99US-0161406.
PR   26-OCT-1999;   99US-0161359.
PR   26-OCT-1999;   99US-0161360.
PR   26-OCT-1999;   99US-0161361.
PR   28-OCT-1999;   99US-0161920.
PR   28-OCT-1999;   99US-0161992.
PR   28-OCT-1999;   99US-0161993.
PR   29-OCT-1999;   99US-0162142.

  Query Match             55.8%;  Score 42.4;  DB 21;  Length 1395;
  Best Local Similarity   72.4%;  Pred. No. 0.00049;
  Matches   55;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy       1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
           |||||  .  || || || || || || || || ||  | |||||| | ||||||||||
Db    1175 AGGTTTCAGAAAACGGCAGCGTATGGACATTTCGGAAGAGACGACCCTGACTTCACCTGG 1234

Qy      61 GAGGTGGTCAAGCCCC 76
           ||||| || ||||| |
Db    1235 GAGGTCGTGAAGCCAC 1250


RESULT 19
AAD22684
ID   AAD22684 standard; DNA; 4848 BP.
XX
AC   AAD22684;
XX
DT   26-FEB-2002  (first entry)
XX
DE   Streptomyces fradiae S-adenosylmethionine (SAM) operon DNA.
XX
KW   S-adenosylmethionine; SAM operon; SAM synthetase; methyltransferase;
KW   MT; methylene tetrahydrofolate reductase; MTHR; activated methyl cycle;
KW   tylosin production; ds.
XX
OS   Streptomyces fradiae.
XX
FH   Key             Location/Qualifiers
FT   CDS             986..2209
FT                   /*tag=  a
FT                   /product= "SAM synthetase protein"
FT   CDS             2241..3341
FT                   /*tag=  b
FT                   /product= "Methyltransferase protein"
FT                   /transl_except= (2241..2243, aa:Met)
FT   CDS             3338..4255
FT                   /*tag=  c
FT                   /product= "Methylene tetrahydrofolate reductase protein"
FT                   /transl_except= (3338..3340, aa:Met)
XX
PN   US6312920-B1.
XX
PD   06-NOV-2001.
XX
PF   22-OCT-1997;   97US-0955957.
XX
PR   13-NOV-1996;   96US-030898P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   DeHoff BS,  Rosteck PR;
XX
DR   WPI; 2002-024904/03.
DR   P-PSDB; AAE13583, AAE13584, AAE13585.
XX
PT   New S-adenosylmethionine (SAM) operon from Streptomyces fradiae which
PT   encodes SAM synthetase, methyltransferase and methylene
PT   tetrahydrofolate reductase, useful for producing SAM by recombinant
PT   techniques -
XX
PS   Claim 19; Column 11-20; 22pp; English.
XX
CC   The patent discloses Streptomyces fradiae S-adenosylmethionine (SAM)
CC   operon which comprises three genes encoding SAM synthetase, methyl-
CC   transferase (MT) and methylene tetrahydrofolate reductase (MTHR).
CC   SAM synthetase, MT and MTHR together comprise the activated methyl
CC   cycle which produces SAM and provides methyl groups required for
CC   the final steps in tylosin production. The invention also relates
CC   to vectors and transformed heterologous host cells for expressing
CC   SAM synthetase. It also relates to a method useful for producing
CC   SAM by recombinant techniques. The present DNA sequence is SAM
CC   operon from Streptomyces fradiae.
XX
SQ   Sequence 4848 BP; 648 A; 1869 C; 1696 G; 635 T; 0 other;

  Query Match             50.3%;  Score 38.2;  DB 24;  Length 4848;
  Best Local Similarity   78.0%;  Pred. No. 0.011;
  Matches   46;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy       4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGA 62
           | |  |||||||||||| |||||||||| ||||| ||     |||| |||||||| ||
Db    2105 TACGCCAAGACCGCCGCCTACGGCCACTTCGGCCGCGAACTGCCCGAGTTCACCTGGGA 2163


RESULT 20
AAD22686
ID   AAD22686 standard; mRNA; 4848 BP.
XX
AC   AAD22686;
XX
DT   26-FEB-2002  (first entry)
XX
DE   Streptomyces fradiae S-adenosylmethionine (SAM) operon mRNA.
XX
KW   S-adenosylmethionine; SAM operon; SAM synthetase; methyltransferase;
KW   MT; methylene tetrahydrofolate reductase; MTHR; activated methyl cycle;
KW   tylosin production; ss.
XX
OS   Streptomyces fradiae.
XX
PN   US6312920-B1.
XX
PD   06-NOV-2001.
XX
PF   22-OCT-1997;   97US-0955957.
XX
PR   13-NOV-1996;   96US-030898P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   DeHoff BS,  Rosteck PR;
XX
DR   WPI; 2002-024904/03.
```

```
XX
PT   New S-adenosylmethionine (SAM) operon from Streptomyces fradiae which
PT   encodes SAM synthetase, methyltransferase and methylene
PT   tetrahydrofolate reductase, useful for producing SAM by recombinant
PT   techniques -
XX
PS   Claim 19; Column 31-36; 22pp; English.
XX
CC   The patent discloses Streptomyces fradiae S-adenosylmethionine (SAM)
CC   operon which comprises three genes encoding SAM synthetase, methyl-
CC   transferase (MT) and methylene tetrahydrofolate reductase (MTHR).
CC   SAM synthetase, MT and MTHR together comprise the activated methyl
CC   cycle which produces SAM and provides methyl groups required for
CC   the final steps in tylosin production. The invention also relates
CC   to vectors and transformed heterologous host cells for expressing
CC   SAM synthetase. It also relates to a method useful for producing
CC   SAM by recombinant techniques. The present mRNA sequence is SAM
CC   operon from Streptomyces fradiae.
XX
SQ   Sequence 4848 BP; 648 A; 1869 C; 1696 G; 635 U; 0 other;

  Query Match             50.3%;  Score 38.2;  DB 24;  Length 4848;
  Best Local Similarity   66.1%;  Pred. No. 0.011;
  Matches   39;  Conservative    7;  Mismatches   13;  Indels    0;  Gaps    0;

Qy       4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGA 62
           : |  |||||||||||| :||||||||:: ||||| ||     |||| ::|||||:| ||
Db    2105 UACGCCAAGACCGCCGCCUACGGCCACUUCGGCCGCGAACUGCCCGAGUUCACCUGGGA 2163


RESULT 21
AAA75637/c
ID   AAA75637 standard; DNA; 1693 BP.
XX
AC   AAA75637;
XX
DT   22-JAN-2001  (first entry)
XX
DE   Nucleotide sequence of ORF15 encoding S-adenosylmethionine synthetase.
XX
KW   Narbonolide synthase; polyketide synthase gene; narbonolide polyketide;
KW   antibiotic; C12-hydroxyalse; picK; desosamine biosynthesis;
KW   desosaminyl transferase enzyme; ketolide; beta-glucosidase enzyme;
KW   picromycin biosynthesis; ss.
XX
OS   Streptomyces venezuelae.
XX
PN   US6117659-A.
XX
PD   12-SEP-2000.
XX
PF   27-MAY-1999;   99US-0320878.
XX
PR   28-MAY-1998;   98US-0087080.
PR   22-SEP-1998;   98US-0100880.
PR   08-FEB-1999;   99US-0119139.
PR   20-MAY-1999;   99US-0134990.
PR   30-APR-1997;   97US-0846247.
PR   06-MAY-1998;   98US-0073538.
PR   28-AUG-1998;   98US-0141908.
XX
PA   (KOSA-) KOSAN BIOSCIENCES INC.
XX
PI   Ashley G,  Betlach MC,  Betlach M,  Tang L,  McDaniel R;
XX
DR   WPI; 2000-610844/58.
XX
PT   New recombinant picK hydroxylase gene of Streptomyces venezuelae useful
PT   for converting ketolides to antibiotics and as antibiotics and
PT   intermediates in the synthesis of compounds with pharmaceutical value
PT   -
XX
PS   Disclosure; Columns 45-46; 117pp; English.
XX
CC   The present sequence is used to produce the recombinant DNA compounds
CC   of the invention. The specification describes a recombinant DNA compound
CC   expressing recombinant polyketide synthase genes in host cells for the
CC   production of narbonolide, narbonolide derivatives and polyketides that
CC   are useful as antibiotics and as intermediates in the synthesis of
CC   compounds with pharmaceutical value. The DNA compounds may also encode
CC   a C12-hydroxyalse (picK), desosamine biosynthesis and desosaminyl
CC   transferase enzymes (useful for conversion of ketolides to antibiotics),
CC   and the beta-glucosidase enzyme (involved in picromycin biosynthesis).
CC   These compounds are also useful for increasing the antibiotic activity
CC   of a compound relative to the unhydroxylated compound. The recombinant
CC   host cells are useful as genetic systems that allow rapid engineering
CC   of the narbonolide polyketide synthase. These would be valuable for
CC   creating novel ketolide analogs for pharmaceutical applications.
XX
SQ   Sequence 1693 BP; 237 A; 566 C; 633 G; 257 T; 0 other;

  Query Match             49.5%;  Score 37.6;  DB 21;  Length 1693;
  Best Local Similarity   76.7%;  Pred. No. 0.015;
  Matches   46;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy       4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           | |  | |||||||||| |||||||||| ||||| ||     | ||||||||||| |||
Db     798 TACTCCCAGACCGCCGCCTACGGCCACTTCGGCCGCGAGCTGCCGGACTTCACCTGGGAG 739


RESULT 22
AAZ56005/c
ID   AAZ56005 standard; DNA; 1693 BP.
XX
AC   AAZ56005;
XX
DT   23-MAR-2000  (first entry)
XX
DE   Contig 004 from cosmid pKOS023-27 from Streptomyces venezuelae.
XX
KW   Narbonolide polyketide synthase; PKS; cosmid pKOS023-27; contig 004;
KW   ketolide; SAM synthase; S-adenosylmethionine synthase; hydroxylase;
KW   picromycin; antibiotic production; narbomycin; ds.
XX
OS   Streptomyces venezuelae.
XX
FH   Key             Location/Qualifiers
FT   CDS             complement (694..1692)
FT                   /*tag= a
FT                   /product= SAM_synthase
FT                   /note= "Partial S-adenosylmethionine synthase"
FT   CDS             complement (3..692)
FT                   /*tag= b
FT                   /product= ORF16_product
FT                   /note= "M. tuberculosis cbhK homologous partial protein"
XX
PN   WO9961599-A2.
XX
PD   02-DEC-1999.
XX
PF   27-MAY-1999;   99WO-US11814.
XX
PR   28-MAY-1998;   98US-0087080.
PR   28-AUG-1998;   98US-0141908.
PR   22-SEP-1998;   98US-0100880.
PR   08-FEB-1999;   99US-0119139.
XX
PA   (KOSA-) KOSAN BIOSCIENCES INC.
XX
PI   Ashley G,  Betlach MC,  Betlach M,  McDaniel R,  Tang L;
XX
DR   WPI; 2000-072618/06.
DR   P-PSDB; AAY67216, AAY67217.
XX
PT   New recombinant DNA encoding a domain of narbonolide polyketide
PT   synthase, for production of ketolide antibiotics -
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```
XX
PS   Disclosure; Page 38; 98pp; English.
XX
CC   This is contig 004 from the recombinant cosmid pKOS023-27 DNA sequence
CC   (see AAZ56001) which contains a Streptomyces venezuelae DNA insert. The
CC   cosmid contains open reading frames which encode the various modules of
CC   the narbonolide polyketide synthase (PKS). The invention relates to
CC   recombinant DNA containing a coding sequence for a narbonolide PKS.
CC   Polyketides are compounds synthesised from 2-carbon units through a
CC   series of condensations and subsequent modifications. Modular PKSs are
CC   responsible for the production of many antibiotics including picromycin.
CC   The narbonolide PKS consists of a loading module, six extender modules,
CC   and two thioester domains. Four proteins make up the narbonolide PKS
CC   (PICAI, PICAII, PICAIII and PICAIV). PICAI includes the loading module
CC   and extender modules 1 and 2, PICAII includes extender modules 3 and 4,
CC   PICAIII includes extender module 5 and PICAIV includes extender module 6
CC   and a type II thioesterase domain. The second type II thioesterase
CC   domain is found on the PICB protein. The nucleotide sequences encoding
CC   all of these proteins can be isolated in recombinant form from the
CC   recombinant cosmid pKOS023-27. Narbonolide is desosaminylated in S.
CC   venezuelae to yield narbomycin, the desosaminyl transferase enzyme is
CC   required for this conversion, and the desosamine biosynthetic genes are
CC   also found in cosmid pKOS023-27. The recombinant DNA of the invention is
CC   used to express, in transformed cells, narbonolide (or its derivatives)
CC   or other ketolides (particularly hybrids), which may then be converted
CC   (e.g. by other enzymes recombinantly expressed in the same hosts) to
CC   polyketide antibiotics or their intermediates. The antibiotics are useful
CC   in human or veterinary medicine.
XX
SQ   Sequence 1693 BP; 237 A; 566 C; 633 G; 257 T; 0 other;

  Query Match             49.5%;  Score 37.6;  DB 21;  Length 1693;
  Best Local Similarity   76.7%;  Pred. No. 0.015;
  Matches   46;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy       4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           | |  | |||||||||| |||||||||| ||||| ||     | |||||||||| |||
Db     798 TACTCCCAGACCGCCGCCTACGGCCACTTCGGCCGCGAGCTGCCGGACTTCACCTGGGAG 739


RESULT 23
ABL72111
ID   ABL72111 standard; cDNA; 297 BP.
XX
AC   ABL72111;
XX
DT   14-MAY-2002  (first entry)
XX
DE   Corn tassel-derived polynucleotide (cdps) SEQ ID NO:1485.
XX
KW   Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPs;
KW   inheritance; characteristic; growth; development; disease resistance;
KW   environmental adaptability; quality; yield; molecular marker;
KW   multigene trait; plant breeding; corn tassel; gene; ss.
XX
OS   Zea mays.
XX
PN   US2001051335-A1.
XX
PD   13-DEC-2001.
XX
PF   16-APR-1999;   99US-0294093.
XX
PR   21-APR-1998;   98US-082567P.
XX
PA   (LALG/) LALGUDI R V.
PA   (ITOL/) ITO L Y.
PA   (SHER/) SHERMAN B K.
XX
PI   Lalgudi RV,  Ito LY,  Sherman BK;
XX
DR   WPI; 2002-163647/21.
XX
PT   Novel purified corn tassel-derived polynucleotide useful for
PT   determining altered gene expression, to recover regulatory elements and
PT   to follow inheritance of desirable characteristics through hybrid
PT   breeding programs -
XX
PS   Claim 1; SEQ ID 1485; 201pp; English.
XX
CC   The present sequence describes a purified corn tassel-derived
CC   polynucleotide sequence (cdps) comprising a nucleic acid sequence
CC   selected from those given in ABL70627 to ABL76833. The cdps sequences
CC   encode corn tassel-derived polypeptides (CDPs). The cdps sequences (I)
CC   can be used for determining altered gene expression, to recover
CC   regulatory elements and to follow inheritance of desirable
CC   characteristics through hybrid breeding programs. (I) are also useful
CC   in the evaluation, and alteration of desired characteristics associated
CC   with growth and development, disease resistance, environmental
CC   adaptability, quality and yield, and as molecular markers for studying
CC   inheritance of multigene traits in a plant breeding program. (I) can be
CC   used to produce a tassel-specific profile of gene transcription, a
CC   transcript image, to clone regulatory elements for use in transformation
CC   vectors, to express a polypeptide, to identify, isolate or extend
CC   identical or related corn tassel nucleic acid sequences from DNA
CC   libraries, in nucleic acid hybridisation or amplification technologies,
CC   as query sequences to determine homology of known sequences, as probe
CC   for use in Southern or Northern hybridisation, and to identify the
CC   presence of and/or to determine the degree of similarity between two
CC   (or more) nucleic acid sequences.
XX
SQ   Sequence 297 BP; 58 A; 85 C; 77 G; 50 T; 27 other;

  Query Match             49.2%;  Score 37.4;  DB 24;  Length 297;
  Best Local Similarity   78.6%;  Pred. No. 0.015;
  Matches   44;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy       2 GGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACC 57
           | | | ||||||| || || |||||| |||||||  | |||||| | |||||||||
Db     242 GCTACCTCAAGACGGCGGCCTACGGCNACTTTGGAAGGGACGACCCTGACTTCACC 297


RESULT 24
AAQ64204
ID   AAQ64204 standard; cDNA; 1208 BP.
XX
AC   AAQ64204;
XX
DT   18-NOV-1994  (first entry)
XX
DE   snaC gene encoding enzyme in streptogramin biosynthetic pathway.
XX
KW   Antibiotic; streptogramin; snaA; snaB; snaC; biosynthesis; enzyme;
KW   biosynthetic pathway; Streptomyces pristinaespiralis; ds.
XX
OS   Streptomyces pristinaespiralis.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1209
FT                   /*tag=  a
XX
PN   FR2696189-A.
XX
PD   01-APR-1994.
XX
PF   25-SEP-1992;   92FR-0011441.
XX
PR   25-SEP-1992;   92FR-0011441.
XX
PA   (RHON ) RHONE POULENC RORER SA.
XX
PI   Blanc V,  Blanche F,  Crouzet J,  Jacques N,  Lacroix P;
PI   Thibaut D,  Zagorec M;
XX
DR   WPI; 1994-128286/16.
DR   P-PSDB; AAR54204.
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```
XX
PT   DNA involved in streptogramin antibiotic biosynthesis - for
PT   prodn. or bio-conversion of streptogramin(s) or prodn. of
PT   streptogramin intermediates, derivs. or hybrid antibiotics
XX
PS   Claim 2; Page 54-55; 83pp; French.
XX
CC   The snaC gene product is involved in the biosynthesis of
CC   streptogramins, antibiotics active against Gram-positive bacteria.
CC   The identification of the sequences encoding the enzymes involved
CC   in the biosynthetic pathway means that they can be isolated and
CC   manipulated.  Mutant microorganisms in which a step in the
CC   streptogramin biosynthetic pathway is blocked can be cultured to
CC   produce streptogramin intermediates, which may later be converted
CC   to streptogramin derivatives.  Recombinant cells may also be used
CC   for the bioconversion of streptogramins from one form to another or
CC   for the production of hybrid antibiotics.
XX
SQ   Sequence 1208 BP; 190 A; 500 C; 360 G; 158 T; 0 other;

  Query Match             49.2%;  Score 37.4;  DB 15;  Length 1208;
  Best Local Similarity   74.6%;  Pred. No. 0.017;
  Matches   47;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy      13 ACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTCAAG 72
           |||||||| |||||||||| ||||| ||     |||||||||||| ||| |  | | |
Db    1114 ACCGCCGCCTACGGCCACTTCGGCCGCGAACTGCCCGACTTCACCTGGGAGCGGACCGAC 1173

Qy      73 CCC 75
           | |
Db    1174 CGC 1176


RESULT 25
AAQ64201
ID   AAQ64201 standard; cDNA; 5392 BP.
XX
AC   AAQ64201;
XX
DT   18-NOV-1994  (first entry)
XX
DE   Sequence comprising the snaA, snaB and snaC gene cluster.
XX
KW   Antibiotic; streptogramin; snaA; snaB; snaC; biosynthesis; enzyme;
KW   biosynthetic pathway; Streptomyces pristinaespiralis; ds.
XX
OS   Streptomyces pristinaespiralis.
XX
PN   FR2696189-A.
XX
PD   01-APR-1994.
XX
PF   25-SEP-1992;   92FR-0011441.
XX
PR   25-SEP-1992;   92FR-0011441.
XX
PA   (RHON ) RHONE POULENC RORER SA.
XX
PI   Blanc V,  Blanche F,  Crouzet J,  Jacques N,  Lacroix P;
PI   Thibaut D,  Zagorec M;
XX
DR   WPI; 1994-128286/16.
XX
PT   DNA involved in streptogramin antibiotic biosynthesis - for
PT   prodn. or bio-conversion of streptogramin(s) or prodn. of
PT   streptogramin intermediates, derivs. or hybrid antibiotics
XX
PS   Disclosure; Page 44-47; 83pp; French.
XX
CC   This sequence comprises the snaA, snaB and snaC genes which are
CC   involved in the biosynthesis of streptogramins, antibiotics active
CC   against Gram-positive bacteria.  The identification of the sequences
CC   encoding the enzymes involved in the biosynthetic pathway means that
CC   they can be isolated and manipulated.  Mutant microorganisms in
CC   which a step in the streptogramin biosynthetic pathway is blocked
CC   can be cultured to produce streptogramin intermediates, which may
CC   later be converted to streptogramin derivatives.  Recombinant cells
CC   may also be used for the bioconversion of streptogramins from one
CC   form to another or for the production of hybrid antibiotics.
XX
SQ   Sequence 5392 BP; 811 A; 2161 C; 1671 G; 749 T; 0 other;

  Query Match             49.2%;  Score 37.4;  DB 15;  Length 5392;
  Best Local Similarity   74.6%;  Pred. No. 0.02;
  Matches   47;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy      13 ACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTCAAG 72
           |||||||| |||||||||| ||||| ||     |||||||||||| ||| |  | | |
Db    4671 ACCGCCGCCTACGGCCACTTCGGCCGCGAACTGCCCGACTTCACCTGGGAGCGGACCGAC 4730

Qy      73 CCC 75
           | |
Db    4731 CGC 4733


RESULT 26
AAI99683
ID   AAI99683 standard; DNA; 4403765 BP.
XX
AC   AAI99683;
XX
DT   15-JAN-2002  (first entry)
XX
DE   Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.
XX
KW   Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
KW   variation; epidemiology; patient treatment; epidemic monitoring; ds.
XX
OS   Mycobacterium tuberculosis.
XX
PN   US6294328-B1.
XX
PD   25-SEP-2001.
XX
PF   24-JUN-1998;   98US-0103840.
XX
PR   24-JUN-1998;   98US-0103840.
XX
PA   (GENO-) INST GENOMIC RES.
XX
PI   Fleischmann RD,  White OR,  Fraser CM,  Venter JC;
XX
DR   WPI; 2001-647261/74.
XX
PT   Evaluating strain variation of Mycobacterium tuberculosis, comprises
PT   determining the nucleotide sequence of the strain at positions in the
PT   genome corresponding to positions where M. tuberculosis strains CDC
PT   1551 and H37Rv differ
XX
PS   Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.
XX
CC   The invention relates to evaluating strain variation within and between
CC   different populations of the tuberculosis bacterial pathogen,
CC   Mycobacterium tuberculosis or related Mycobacterium by determining the
CC   nucleotide sequence of the first strain at positions in the complete
CC   sequence of the genome that correspond to positions that differ in the
CC   nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and
CC   H37Rv (AAI99682). The method is useful for evaluating strain variation of
CC   M. tuberculosis and has valuable application in the fields of
CC   tuberculosis genetics, epidemiology, patient treatment and epidemic
CC   monitoring.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from USPTO
CC   at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
XX
SQ   Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
```

```
  Query Match             45.3%;  Score 34.4;  DB 22;  Length 4403765;
  Best Local Similarity   73.3%;  Pred. No. 0.31;
  Matches   44;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy      12 GACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTCAA 71
           |||||||||| ||||| ||||| |||||   ||||| ||| ||  | || |||  | || |
Db 1567783 GACCGCCGCCTACGGGCACTTCGGCCGCACCGACGTCGAATTACCGTGGGAGCAGCTCGA 1567842


RESULT 27
AAI99682
ID   AAI99682 standard; DNA; 4411529 BP.
XX
AC   AAI99682;
XX
DT   15-JAN-2002  (first entry)
XX
DE   Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.
XX
KW   Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
KW   variation; epidemiology; patient treatment; epidemic monitoring; ds.
XX
OS   Mycobacterium tuberculosis.
XX
PN   US6294328-B1.
XX
PD   25-SEP-2001.
XX
PF   24-JUN-1998;   98US-0103840.
XX
PR   24-JUN-1998;   98US-0103840.
XX
PA   (GENO-) INST GENOMIC RES.
XX
PI   Fleischmann RD,  White OR,  Fraser CM,  Venter JC;
XX
DR   WPI; 2001-647261/74.
XX
PT   Evaluating strain variation of Mycobacterium tuberculosis, comprises
PT   determining the nucleotide sequence of the strain at positions in the
PT   genome corresponding to positions where M. tuberculosis strains CDC
PT   1551 and H37Rv differ  -
XX
PS   Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.
XX
CC   The invention relates to evaluating strain variation within and between
CC   different populations of the tuberculosis bacterial pathogen,
CC   Mycobacterium tuberculosis or related Mycobacterium by determining the
CC   nucleotide sequence of the first strain at positions in the complete
CC   sequence of the genome that correspond to positions that differ in the
CC   nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and
CC   H37Rv (AAI99682). The method is useful for evaluating strain variation of
CC   M. tuberculosis and has valuable application in the fields of
CC   tuberculosis genetics, epidemiology, patient treatment and epidemic
CC   monitoring.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from USPTO
CC   at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
XX
SQ   Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;

  Query Match             45.3%;  Score 34.4;  DB 22;  Length 4411529;
  Best Local Similarity   73.3%;  Pred. No. 0.31;
  Matches   44;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy      12 GACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTCAA 71
           |||||||||| ||||| ||||| |||||   ||||| ||| ||  | || |||  | || |
Db 1567944 GACCGCCGCCTACGGGCACTTCGGCCGCACCGACGTCGAATTACCGTGGGAGCAGCTCGA 1568003


RESULT 28
AAA81476
ID   AAA81476 standard; DNA; 56485 BP.
XX
AC   AAA81476;
XX
DT   04-DEC-2000  (first entry)
XX
DE   N. meningitidis partial DNA sequence gnm_24 SEQ ID NO:24.
XX
KW   Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic;
KW   antigen; vaccine; diagnosis; infection; antibacterial; identification;
KW   Meningococcus B; MenB; ds.
XX
OS   Neisseria meningitidis.
XX
PN   WO200022430-A2.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-US23573.
XX
PR   09-OCT-1998;   98US-0103794.
PR   30-APR-1999;   99US-0132068.
XX
PA   (CHIR ) GHIRON CORP.
XX
PI   Frazer CM,  Hickey E,  Peterson J,  Tettelin H,  Venter JC;
PI   Masignani V,  Galeotti C,  Mora M,  Ratti G,  Scarselli M,  Scarlato V;
PI   Rappuoli R,  Pizza M;
XX
DR   WPI; 2000-318079/27.
XX
PT   Isolated nucleotide sequences of Neisseria meningitidis which can be
PT   used in the diagnosis and treatment of N. meningitidis infection and
PT   other Neisserial infections, for example, N.gonorrhoea -
XX
PS   Claim 7; Page 507-524; 1760pp; English.
XX
CC   The present invention describes methods of obtaining immunogenic
CC   proteins from Neisseria genomic sequences. AAA81453 to AAA82414
CC   represent specifically claimed Neisseria meningitidis genomic DNA
CC   sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
CC   Neisseria DNA sequences and their corresponding proteins; AAA81254 to
CC   AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
CC   isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
CC   AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
CC   sequences, which are all used in the exemplification of the present
CC   invention. The nucleic acid sequences, protein sequences, and antibodies
CC   against them, can be used in the manufacture of a composition. The
CC   composition can be used as a medicament (or in the manufacture of a
CC   medicament) for treating, preventing or diagnosing infection due to
CC   Neisserial bacteria. For example, some of the identified proteins could
CC   be components of vaccines against Meningococcus B; against all serotypes;
CC   and/or against all pathogenic Neissariae. Identification of sequences
CC   from the bacterium will also facilitate production of biological probes,
CC   particularly organism-specific probes. Attempts to make efficacious
CC   Meningococcus B vaccines have failed mainly due to antigen tolerance.
CC   Multivalent vaccines have also been tried but none have successfully
CC   overcome antigenic variability. The provision of further, complete
CC   sequences may provide an opportunity to identify secreted or surface
CC   exposed proteins that may be presumed targets for the immune system and
CC   which are not antigenically variable or at least more conserved than
CC   other more variable regions.
XX
SQ   Sequence 56485 BP; 12504 A; 14247 C; 16158 G; 13573 T; 3 other;

  Query Match             43.2%;  Score 32.8;  DB 21;  Length 56485;
  Best Local Similarity   71.7%;  Pred. No. 0.67;
  Matches   43;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy       4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           | ||  ||  ||||||| ||||| || || ||||| || ||  | || ||||| || |||
Db   54065 TACAGTAAATCCGCCGCTTACGGACATTTCGGCCGCGAAGAACCTGAGTTCACTTGGGAG 54124
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RESULT 29
AAF21612/c
ID   AAF21612 standard; DNA; 349980 BP.
XX
AC   AAF21612;
XX
DT   13-MAR-2001  (first entry)
XX
DE   Neisseria meningitidis B nucleotide sequence SEQ ID NO:113.
XX
KW   Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine;
KW   diagnosis; antigen; detection; infection; gene therapy; antibacterial;
KW   ds.
XX
OS   Neisseria meningitidis.
XX
PN   WO200066791-A1.
XX
PD   09-NOV-2000.
XX
PF   08-MAR-2000; 2000WO-US05928.
XX
PR   30-APR-1999;   99US-0132068.
PR   08-OCT-1999;   99WO-US23573.
PR   28-FEB-2000; 2000GB-0004695.
XX
PA   (CHIR ) CHIRON CORP.
PA   (GENO-) INST GENOMIC RES.
XX
PI   Pizza M,  Hickey E,  Peterson J,  Tettelin H,  Venter JC,  Masignani V;
PI   Galeotti C,  Mora M,  Ratti G,  Scarselli M,  Scarlato V,  Rappuoli R;
PI   Frazer CM,  Grandi G;
XX
DR   WPI; 2000-647603/62.
XX
PT   Neisseria meningitidis B full length genome sequence and open reading
PT   frames are used to detect, treat and prevent Neisserial infections -
XX
PS   Claim 7; Appendix A; 692pp; English.
XX
CC   The present invention describes the full length genome of
CC   Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607
CC   to AAF21613 represent fragments of the NMB genomic sequence, as the
CC   sequence was too long to go in a record on its own it was split into 8
CC   sequences which overlap each other at the beginning and end of each
CC   sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at
CC   the beginning  of AAF21607, the last 49980 bp of AAF21607 are repeated at
CC   the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the
CC   Neisseria proteins given in AAB58550 to AAB58593, and AAF21589 to
CC   AAF21606 represent PCR primers which are used in the exemplification of
CC   the present invention. The NMB genome and fragments from it have
CC   antibacterial activity, and can be used in vaccines and gene therapy.
CC   Neisseria nucleic acids, proteins and/or antibodies which binds to the
CC   proteins can be used in compositions for treating or preventing infection
CC   due to Neisserial bacteria or as a diagnostic reagent for detecting the
CC   presence of Neisserial bacteria or of antibodies raised to Neisserial
CC   bacteria. Computers, computer memory, computer storage medium or computer
CC   databases can be used in a search to identify open reading frames (ORFs)
CC   or coding sequences within the NMB genome. The DNA sequences provide
CC   further opportunities to find antigenic or immunogenic proteins which are
CC   more effective in vaccines than the outer membrane proteins currently
CC   used.
XX
SQ   Sequence 349980 BP; 86473 A; 95646 C; 85908 G; 81953 T; 0 other;

  Query Match             43.2%;  Score 32.8;  DB 21;  Length 349980;
  Best Local Similarity   71.7%;  Pred. No. 0.79;
  Matches   43;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy       4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           | ||  ||  ||||||| ||||| || || ||||| || ||  | || ||||| || |||
Db   87589 TACAGTAAATCCGCCGCTTACGGACATTTCGGCCGCGAAGAACCTGAGTTCACTTGGGAG 87530
```

```
RESULT 30
AAA81489/c
ID   AAA81489 standard; DNA; 837096 BP.
XX
AC   AAA81489;
XX
DT   04-DEC-2000  (first entry)
XX
DE   N. meningitidis partial DNA sequence gnm_37 SEQ ID NO:37.
XX
KW   Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic;
KW   antigen; vaccine; diagnosis; infection; antibacterial; identification;
KW   Meningococcus B; MenB; ds.
XX
OS   Neisseria meningitidis.
XX
PN   WO200022430-A2.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-US23573.
XX
PR   09-OCT-1998;   98US-0103794.
PR   30-APR-1999;   99US-0132068.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Frazer CM,  Hickey E,  Peterson J,  Tettelin H,  Venter JC;
PI   Masignani V,  Galeotti C,  Mora M,  Ratti G,  Scarselli M,  Scarlato V;
PI   Rappuoli R,  Pizza M;
XX
DR   WPI; 2000-318079/27.
XX
PT   Isolated nucleotide sequences of Neisseria meningitidis which can be
PT   used in the diagnosis and treatment of N. meningitidis infection and
PT   other Neisserial infections, for example, N.gonorrhoea -
XX
PS   Claim 7; Page 629-865; 1760pp; English.
XX
CC   The present invention describes methods of obtaining immunogenic
CC   proteins from Neisseria genomic sequences. AAA81453 to AAA82414
CC   represent specifically claimed Neisseria meningitidis genomic DNA
CC   sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
CC   Neisseria DNA sequences and their corresponding proteins; AAA81254 to
CC   AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
CC   isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
CC   AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
CC   sequences, which are all used in the exemplification of the present
CC   invention. The nucleic acid sequences, protein sequences, and antibodies
CC   against them, can be used in the manufacture of a composition. The
CC   composition can be used as a medicament (or in the manufacture of a
CC   medicament) for treating, preventing or diagnosing infection due to
CC   Neisserial bacteria. For example, some of the identified proteins could
CC   be components of vaccines against Meningococcus B; against all serotypes;
CC   and/or against all pathogenic Neissariae. Identification of sequences
CC   from the bacterium will also facilitate production of biological probes,
CC   particularly organism-specific probes. Attempts to make efficacious
CC   Meningococcus B vaccines have failed mainly due to antigen tolerance.
CC   Multivalent vaccines have also been tried but none have successfully
CC   overcome antigenic variability. The provision of further, complete
CC   sequences may provide an opportunity to identify secreted or surface
CC   exposed proteins that may be presumed targets for the immune system and
CC   which are not antigenically variable or at least more conserved than
CC   other more variable regions.
XX
SQ   Sequence 837096 BP; 207534 A; 227065 C; 205215 G; 197280 T; 2 other;

  Query Match             43.2%;  Score 32.8;  DB 21;  Length 837096;
  Best Local Similarity   71.7%;  Pred. No. 0.85;
  Matches   43;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;
```

```
Qy       4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
Db 452360 TACAGTAAATCCGCCGCTTACGGACATTTCGGCCGCGAAGAACCTGAGTTCACTTGGGAG 452301
```

RESULT 31
AAS51580/c
ID AAS51580 standard; DNA; 606 BP.
XX
AC AAS51580;
XX
DT 13-FEB-2002 (first entry)
XX
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #165.
XX
KW Antisense; ds; prokaryotic cellular proliferation gene;
KW antibiotic; antibacterial; drug design.
XX
OS Pseudomonas aeruginosa.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR P-PSDB; AAU33721.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
PS Claim 27; Seq ID No 4162; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence encodes an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 606 BP; 121 A; 212 C; 185 G; 88 T; 0 other;

Query Match 40.3%; Score 30.6; DB 23; Length 606;
Best Local Similarity 68.9%; Pred. No. 2.1;
Matches 42; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

```
Qy      15 CGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTCAAGCC 74
Db     106 CGCCGCATACCGCGGCTTTCGCCTGGCCCGCGGCGGCATCGCCAGCGGCATGGGCAAGGC 47

Qy      75 C 75
           |
Db      46 C 46
```

RESULT 32
AAF12426
ID AAF12426 standard; cDNA; 657 BP.
XX
AC AAF12426;
XX
DT 13-MAR-2001 (first entry)
XX
DE Aspergillus oryzae EST SEQ ID NO:4949.
XX
KW Multiple gene expression; filamentous fungal cell; EST;
KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;
KW culture condition; environmental stress; spore morphogenesis;
KW metabolic pathway engineering; catabolic pathway engineering; ss.
XX
OS Aspergillus oryzae.
XX
PN WO200056762-A2.
XX
PD 28-SEP-2000.
XX
PF 22-MAR-2000; 2000WO-US07781.
XX
PR 22-MAR-1999; 99US-0273623.
XX
PA (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO NORDISK AS.
XX
PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
XX
DR WPI; 2000-594572/56.
XX
PT Monitoring differential expression of genes in filamentous fungal cells
PT uses fluorescence-labeled nucleic acids isolated from the cells and a
PT substrate of expressed sequence tags -
XX
PS Claim 88; Page 2084; 3161pp; English.
XX
CC The present invention describes a method for monitoring differential
CC expression of genes in a first filamentous fungal (FF) cell relative to
CC expression of the same genes in one or more second filamentous fungal
CC cells. The method uses fluorescence-labeled nucleic acids isolated from
CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
CC are used in the methods for monitoring differential expression of genes
CC in a first filamentous fungal (FF) cell relative to expression of the
CC same genes in one or more second filamentous fungal cells. Monitoring
CC the global expression of genes from FF cells allows the production
CC potential of the microorganisms to be improved. New genes may be
CC discovered, possible functions of unknown open reading frames can be
CC identified and gene copy number variation and stability can be
CC monitored. The expression of genes can be used to study how FF cells
CC adapt to changes in culture conditions, environmental stress, spore
CC morphogenesis, recombination, metabolic or catabolic pathway
CC engineering. Using ESTs provides several advantages over genomic or
CC random cDNA clones including elimination of redundancy as one spot on an
CC array equals one gene or open reading frame, and organisation of the
CC microarrays based on function of the gene products to facilitate
CC analysis of the results. AAF07478 to AAF11247 represents ESTs from
CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
CC all specifically claimed in the present invention.
XX

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SQ   Sequence 657 BP; 155 A; 175 C; 134 G; 193 T; 0 other;

  Query Match             37.6%;  Score 28.6;  DB 21;  Length 657;
  Best Local Similarity   61.3%;  Pred. No. 9;
  Matches   46;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy       1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
           | |  |||  |   ||||| |   ||| | ||||    |||| ||| |||  | ||| ||
Db     221 ATGGGCATTGACGACGCCGAAATTGGCGAGTTTGCTTATGACTACGTCGAGATTACCCGC 280

Qy      61 GAGGTGGTCAAGCCC 75
           || ||| |||   ||
Db     281 GACGTGATCAGTGCC 295


RESULT 33
AAF08609
ID   AAF08609 standard; cDNA; 383 BP.
XX
AC   AAF08609;
XX
DT   13-MAR-2001  (first entry)
XX
DE   Fusarium venenatum EST SEQ ID NO:1132.
XX
KW   Multiple gene expression; filamentous fungal cell; EST;
KW   expressed sequence tag; Fusarium venenatum; Aspergillus niger;
KW   Aspergillus oryzae; Trichoderma reesei; identification; recombination;
KW   culture condition; environmental stress; spore morphogenesis;
KW   metabolic pathway engineering; catabolic pathway engineering; ss.
XX
OS   Fusarium venenatum.
XX
PN   WO200056762-A2.
XX
PD   28-SEP-2000.
XX
PF   22-MAR-2000; 2000WO-US07781.
XX
PR   22-MAR-1999;   99US-0273623.
XX
PA   (NOVO ) NOVO NORDISK BIOTECH INC.
PA   (NOVO ) NOVO NORDISK AS.
XX
PI   Berka RM,  Rey MW,  Shuster JR,  Kauppinen S,  Clausen IG,  Olsen PB;
XX
DR   WPI; 2000-594572/56.
XX
PT   Monitoring differential expression of genes in filamentous fungal cells
PT   uses fluorescence-labeled nucleic acids isolated from the cells and a
PT   substrate of expressed sequence tags -
XX
PS   Claim 86; Page 813; 3161pp; English.
XX
CC   The present invention describes a method for monitoring differential
CC   expression of genes in a first filamentous fungal (FF) cell relative to
CC   expression of the same genes in one or more second filamentous fungal
CC   cells. The method uses fluorescence-labeled nucleic acids isolated from
CC   the FF cells and a substrate of expressed sequence tags (EST). The ESTs
CC   are used in the methods for monitoring differential expression of genes
CC   in a first filamentous fungal (FF) cell relative to expression of the
CC   same genes in one or more second filamentous fungal cells. Monitoring
CC   the global expression of genes from FF cells allows the production
CC   potential of the microorganisms to be improved. New genes may be
CC   discovered, possible functions of unknown open reading frames can be
CC   identified and gene copy number variation and stability can be
CC   monitored. The expression of genes can be used to study how FF cells
CC   adapt to changes in culture conditions, environmental stress, spore
CC   morphogenesis, recombination, metabolic or catabolic pathway
CC   engineering. Using ESTs provides several advantages over genomic or
CC   random cDNA clones including elimination of redundancy as one spot on an
CC   array equals one gene or open reading frame, and organisation of the
CC   microarrays based on function of the gene products to facilitate
CC   analysis of the results. AAF07478 to AAF11247 represents ESTs from
CC   Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
CC   niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
CC   AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
CC   all specifically claimed in the present invention.
XX
SQ   Sequence 383 BP; 74 A; 115 C; 87 G; 89 T; 18 other;

  Query Match             36.6%;  Score 27.8;  DB 21;  Length 383;
  Best Local Similarity   61.1%;  Pred. No. 15;
  Matches   44;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy       4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           | | |  ||| |  |||    | | |||||| ||| | || ||||| |  |||| | ||
Db     145 TACTTTGAGAACCTCGCTCCTGTCNACTTTGCCCGCGCCGGCGCCGTCGCCACCCGAGAC 204

Qy      64 GTGGTCAAGCCC 75
             |  |||  |||
Db     205 TTCTTCATTCCC 216


RESULT 34
ABK13571
ID   ABK13571 standard; cDNA; 2284 BP.
XX
AC   ABK13571;
XX
DT   23-APR-2002  (first entry)
XX
DE   Ryegrass 4-coumarate Co-A-ligase 1 (Lp4CL1) cDNA.
XX
KW   Perennial ryegrass; ss; lignin; 4 coumarate CoA-ligase; QTL; gene;
KW   lignin biosynthesis; enzyme; cinnamoyl-CoA reductase; CCR; Lp4CL1;
KW   cinnamyl alcohol dehydrogenase; CAD; molecular genetic marker;
KW   qualitative trait loci; tagging; QTL mapping; DNA fingerprinting;
KW   marker assisted selection; forage improvement; turf grass improvement;
KW   dry matter digestibility; herbage quality; palatability; regrowth;
KW   cold tolerance; drought tolerance; tiller survival; plant persistence.
XX
OS   Lolium perenne.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..322
FT                   /*tag= a
FT   CDS             323..2146
FT                   /*tag= b
FT                   /product= "LP4CL1 protein"
FT                   /transl_except= (pos:2030..2038, aa:Ala Arg)
FT   3'UTR           2147..2266
FT                   /*tag= c
FT   polyA_site      2267..2284
FT                   /*tag= d
XX
PN   WO200195702-A1.
XX
PD   20-DEC-2001.
XX
PF   14-JUN-2001; 2001WO-AU00699.
XX
PR   14-JUN-2000; 2000AU-0008154.
XX
PA   (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.
PA   (UYAD-) UNIV ADELAIDE.
PA   (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
PA   (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
PA   (UYSC-) UNIV SOUTHERN CROSS.
PA   (DAIR-) DAIRY RES & DEV CORP.
XX
PI   Spangenberg GC,  Lidgett AJ,  Heath RL,  Mcinnes RL,  Lynch DP;
XX
DR   WPI; 2002-097993/13.
DR   P-PSDB; AAU75084.
XX
```

PT Novel nucleic acid encoding enzymes involved in lignin biosynthetic
PT pathway from ryegrass or fescue species useful for modifying lignin
PT biosynthesis in plants and as a molecular genetic marker -
XX
PS Claim 3; Fig 2; 148pp; English.
XX
CC This invention represents purified or isolated nucleic acid and protein
CC sequences of enzymes involved in lignin biosynthesis. The enzymes
CC of the invention are 4 coumarate CoA-ligase (4CL), cinnamoyl-CoA
CC reductase (CCR) and cinnamyl alcohol dehydrogenase (CAD) from a ryegrass
CC (Lolium sp.) or fescue (Festuca sp.). The invention also comprises an
CC isolated regulatory element from the nucleic acid sequences and a plant
CC cell or seed transformed with the nucleic acid. An isolated regulatory
CC element from these nucleotide molecules is useful for expressing an
CC exogenous gene in plant cells. The nucleotide sequences of the invention
CC and vectors containing these sequences are useful for modifying lignin
CC biosynthesis in a plant and are useful as a molecular genetic marker for
CC qualitative trait loci (QTL) tagging, QTL mapping, DNA fingerprinting
CC and in marker assisted selection, in forage and turf grass improvement,
CC e.g. tagging QTLs for dry matter digestibility, herbage quality,
CC palatability, regrowth after cutting and grazing, cold tolerance,
CC drought tolerance, tiller survival and plant persistence. The present
CC sequence represents the perennial ryegrass 4-coumarate Co-A-ligase 1
CC (Lp4CL1) cDNA of the invention.
XX
SQ Sequence 2284 BP; 391 A; 750 C; 733 G; 410 T; 0 other;

Query Match 36.6%; Score 27.8; DB 24; Length 2284;
Best Local Similarity 62.0%; Pred. No. 18;
Matches 44; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

```
Qy      2 GGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCG 61
          |||   || | |||| ||    |||| || | | |   ||||||| | ||||| |  ||
Db   1647 GGTGGCTCCACACCGGCGACATCGGCTACGTCGACGACGACGACGAGGTCTTCATCGTCG 1706

Qy     62 AGGTGGTCAAG 72
          |    ||||||
Db   1707 ACCGCGTCAAG 1717
```

RESULT 35
AAT13227
ID AAT13227 standard; DNA; 3600 BP.
XX
AC AAT13227;
XX
DT 16-SEP-1996 (first entry)
XX
DE Thermostable enzyme (converting maltose to trehalose) DNA.
XX
KW Thermostable enzyme; thermophilic bacterium; sweetener; trehalose;
KW maltose; food; recombinant enzyme; cosmetic; pharmaceutical; ds.
XX
OS Thermus aquaticus ATCC 33923.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..540
FT /*tag= a
FT mat_peptide 541..3429
FT /*tag= b
FT 3'UTR 3430..3600
FT /*tag= c
XX
PN EP704531-A2.
XX
PD 03-APR-1996.
XX
PF 29-SEP-1995; 95EP-0306875.
XX
PR 08-SEP-1995; 95JP-0255829.
PR 01-OCT-1994; 94JP-0260984.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Kubota M, Sugimoto T, Tsusaki K;
XX
DR WPI; 1996-173035/18.
DR P-PSDB; AAR84081, AAR84082.
XX
PT Isolated DNA encoding enzyme for converting maltose to trehalose -
PT used for prodn. of trehalose for use in food prods., cosmetics and
PT pharmaceuticals, partic. as sweetener
XX
PS Claim 8; Page 28-31; 46pp; English.
XX
CC This DNA encoding a thermostable enzyme which converts maltose to
CC trehalose may be used to express the enzyme recombinantly in E. coli
CC using plasmid vector Bluescript II SK(+) or plasmid pKK223-3. The
CC enzyme is then produced by culturing the transformant. The enzyme
CC catalyses a reaction to produce high yields of trehalose at high
CC temp., which prevents bacterial contamination. Trehalose is used in
CC food products, cosmetics and pharmaceuticals, as a sweetener, etc.
XX
SQ Sequence 3600 BP; 559 A; 1346 C; 1168 G; 527 T; 0 other;

Query Match 36.6%; Score 27.8; DB 17; Length 3600;
Best Local Similarity 62.0%; Pred. No. 19;
Matches 44; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

```
Qy      2 GGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCG 61
          || ||  | | ||||||   |  | || |||   |||  || ||| |||  |||||   |
Db   1412 GGATCCCCGAAACCGCCCAGTGGGCCCTCTTCCTCCGCAACCACGACGAGCTCACCCTGG 1471

Qy     62 AGGTGGTCAAG 72
          ||  ||||| |
Db   1472 AGAAGGTCACG 1482
```

RESULT 36
AAX19362
ID AAX19362 standard; DNA; 7584 BP.
XX
AC AAX19362;
XX
DT 19-MAY-1999 (first entry)
XX
DE Rhodococcus corallina ohp operon.
XX
KW Rhodococcus corallina; ohp operon; biosensor; mycolic acid bacteria;
KW inducible promoter; environmental pollutant; industry; medicine; ds.
XX
OS Rhodococcus corallina.
XX
PN WO9900517-A2.
XX
PD 07-JAN-1999.
XX
PF 29-JUN-1998; 98WO-GB01893.
XX
PR 27-JUN-1997; 97GB-0013666.
XX
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
PI Archer JAC, Powell JAC, Roland HJ, Summers DK;
XX
DR WPI; 1999-095760/08.
DR P-PSDB; AAW99181, AAW99182, AAW99183, AAW99184, AAW99185, AAW99186.
XX
PT Isolating DNA encoding inducible promoter from mycolic acid bacteria
PT - useful to produce mycolic acid bacterial biosensors for particular
PT analytes, such as environmental pollutants, e.g. from industry or
PT medicine
XX
PS Example 7; Fig 4; 67pp; English.
XX
CC A method has been developed for identifying and/or isolating DNA from

```
CC   mycolic acid bacteria which encodes an inducible promoter induced in
CC   response to a particular analyte (and/or associated operon proteins).
CC   The method comprises: (a) culturing source of mycolic acid bacteria in
CC   selective media containing specific analyte and selective for
CC   oligotrophic bacteria; (b) identifying mycolic acid bacteria subsisting
CC   on medium; (c) extracting DNA from these bacteria; (d) incorporating DNA
CC   into vector; (e) cloning vector into suitable host cell; and (f)
CC   screening host cells for inducible promoter and/or proteins to identify
CC   vectors encoding it. The method allows isolation of DNA encoding a
CC   promoter which is induced in response to a particular analyte (and/or
CC   associated operon proteins), which can be used to produce biosensors for
CC   the analyte. The DNA is incorporated into vectors which are used to
CC   transform host cells to produce the biosensors. It is especially useful
CC   when the analyte is an environmental pollutant (e.g. from industry or
CC   medicine), especially a hydrophic organic compound such as components of
CC   fuels, pesticides; the biosensors may then be used to detect small
CC   concentrations of analytes in samples e.g. for pollution monitoring. The
CC   identified DNA can also be modified to produce modified inducible
CC   promoters and/or operons also useful in biosensor production. The method
CC   allows rapid isolation of promoters (and/or operon proteins) whist
CC   minimising host restrictions (e.g. thick cell walls of mycolic acid
CC   bacteria which confer resistance to cell lysis) and requiring no
CC   knowledge of inducible enzyme chemistry involved (which may be unknown
CC   for specific analyte). The present sequence represents the R. corallina
CC   ohp operon, given in the present invention.
XX
SQ   Sequence 7584 BP; 1329 A; 2735 C; 2286 G; 1234 T; 0 other;

  Query Match             36.6%;  Score 27.8;  DB 20;  Length 7584;
  Best Local Similarity   69.1%;  Pred. No. 20;
  Matches   38;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy      15 CGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTC 69
           |||||||| || ||||    ||||   || ||||||||||  ||  |||  |  ||
Db    5804 CGCCGCATTCGACCACGCGCGCCGGTTCGTCGCCGACTTCGCCCCCGATCTCATC 5858


RESULT 37
AAA51878
ID   AAA51878 standard; DNA; 7600 BP.
XX
AC   AAA51878;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Rhodococcus sp. OHP operon.
XX
KW   OHP operon; orthohydroxyphenylpropionic acid; regulator; inducible;
KW   gene expression system; plant transformation; ds.
XX
OS   Rhodococcus sp. V49.
XX
FH   Key             Location/Qualifiers
FT   CDS             296..1036
FT                   /*tag=  a
FT                   /product= ohpH_regulator
FT   CDS             1262..2806
FT                   /*tag=  b
FT                   /product= ohpA_transport_protein
FT   CDS             2808
FT                   /*tag=  c
FT   CDS             ..4721
FT                   /*tag=  d
FT                   /product= ohpB_monooxygenase
FT   CDS             5722..6666
FT                   /*tag=  e
FT                   /product= ohpD_catechol_2,3-dioxygenase
XX
PN   WO200039300-A1.
XX
PD   06-JUL-2000.
XX
PF   21-DEC-1999;   99WO-GB04333.
XX
PR   24-DEC-1998;   98GB-0028660.
XX
PA   (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
PI   Tuerck JA,  Archer JAC;
XX
DR   WPI; 2000-452398/39.
DR   P-PSDB; AAY97050, AAY97051, AAY97051, AAY97052, AAY97053.
XX
PT   New chimaeric gene for controlling eukaryotic gene expression or
PT   transforming plant tissue of monocot or a dicot crops, trees or other
PT   plants, comprises regulatory regions for a regulator polypeptide and a
PT   nucleic acid
XX
PS   Claim 30; Page 91-100; 114pp; English.
XX
CC   This is the OHP (orthohydroxyphenylpropionic acid) operon from
CC   Rhodococcus sp. V49. The OPH responsive regulator polypeptide coding
CC   sequence can be used in novel chimaeric genes for use in chemically
CC   inducible gene expression systems. The chimaeric gene comprises a
CC   promoter and a regulator polypeptide coding sequence linked with a
CC   second sequence comprising a promoter and a coding or non-coding
CC   sequence. Expression of the target gene of the second sequence is
CC   controlled by the regulatory polypeptide which is acted upon by an
CC   inducer. The chimaeric gene is used to control eukaryotic gene
CC   expression or transform plant tissue of monocot or a dicot crops, trees
CC   or other plants, such as potato, wheat, maize, barley, tomato, rice,
CC   canola, sugarbeet, tobacco, eucalyptus, populus, malus, or Arabidopsis.
CC   Carbon metabolism, flowering, fertility and/or sterility, cell wall
CC   metabolism, genes that respond to environmental signals, such as pathogen
CC   attack, bacterium, fungus, virus, or insect resistance, or genes that
CC   confer resistance to antibiotics, herbicides or other toxic compounds can
CC   be controlled (all claimed).
XX
SQ   Sequence 7600 BP; 1332 A; 2742 C; 2289 G; 1237 T; 0 other;

  Query Match             36.6%;  Score 27.8;  DB 21;  Length 7600;
  Best Local Similarity   69.1%;  Pred. No. 20;
  Matches   38;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy      15 CGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTC 69
           |||||||| || ||||    ||||   || ||||||||||  ||  |||  |  ||
Db    5805 CGCCGCATTCGACCACGCGCGCCGGTTCGTCGCCGACTTCGCCCCCGATCTCATC 5859


RESULT 38
AAD07974
ID   AAD07974 standard; cDNA; 1957 BP.
XX
AC   AAD07974;
XX
DT   06-AUG-2001  (first entry)
XX
DE   Rice cysteinyl-tRNA synthetase cDNA clone rs11n.pk016.p18.
XX
KW   Rice; cysteinyl-tRNA synthetase; herbicide; genetic mapping;
KW   plant breeding; ss.
XX
OS   Oryza sativa.
XX
FH   Key             Location/Qualifiers
FT   CDS             3..1649
FT                   /*tag=  a
FT                   /product= "Cysteinyl-tRNA synthetase"
FT                   /note= "CDS does not include start codon"
FT                   /partial
XX
PN   US6255090-B1.
XX
PD   03-JUL-2001.
XX
PF   14-JUL-1999;   99US-0352990.
```

```
XX
PR   15-JUL-1998;   98US-0092866.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Famodu LO,  Orozco EM,  Rafalski JA;
XX
DR   WPI; 2001-388927/41.
DR   P-PSDB; AAE03590.
XX
PT   New isolated polynucleotide encoding an aspartyl-tRNA synthetase useful
PT   as targets to facilitate design and/or identification of inhibitors of
PT   those enzymes that may be useful as herbicides -
XX
PS   Example 4; Column 39-42; 40pp; English.
XX
CC   The present sequence is a cDNA encoding rice cysteinyl-tRNA synthetase
CC   of the invention. The cysteinyl-tRNA synthetase are used as targets to
CC   facilitate designing and identification of inhibitors of the enzymes
CC   which are useful as herbicides. All or a substantial portion of the
CC   nucleic acid fragments of the present invention are used as probes for
CC   genetically and physically mapping the genes that they are a part of,
CC   and as markers for traits linked to those genes. Such information is
CC   useful in plant breeding in order to develop lines with desired
CC   phenotypes.
XX
SQ   Sequence 1957 BP; 599 A; 384 C; 470 G; 504 T; 0 other;

  Query Match             36.3%;  Score 27.6;  DB 22;  Length 1957;
  Best Local Similarity   63.6%;  Pred. No. 20;
  Matches   42;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy       6 CATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGT 65
           | ||| | ||  ||  | | ||||| | ||||  | |  |||| || || ||| ||| ||
Db     176 CGTCACGCCCTACGACTTCAGCCACATCGGCCACGCCCGCGCCTACGTCGCCTTCGACGT 235

Qy      66 GGTCAA 71
             || |
Db     236 CCTCTA 241


RESULT 39
ABQ90584
ID   ABQ90584 standard; DNA; 2907 BP.
XX
AC   ABQ90584;
XX
DT   01-OCT-2002  (first entry)
XX
DE   M. capsulatus gene #569 for DNA array.
XX
KW   Micro array; gene; ds; differential expression; gene expression.
XX
OS   Methylococcus capsulatus.
XX
PN   WO200255655-A2.
XX
PD   18-JUL-2002.
XX
PF   14-JAN-2002; 2002WO-NO00019.
XX
PR   12-JAN-2001; 2001NO-0000235.
PR   12-JAN-2001; 2001NO-0000239.
XX
PA   (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN.
PA   (TIGR-) TIGR.
XX
PI   Birkeland NK,  Eidhammer I,  Jonassen I,  Jensen HB,  Lien T;
PI   Lillehaug JR,  Lossius I,  Eisen JA,  Fraser CM,  Durkin AS;
PI   Salzberg SL;
XX
DR   WPI; 2002-557818/59.
XX
PT   Novel DNA array useful for determining differential expression of
PT   Methylococcus capsulatus genes, comprises polynucleotides or
PT   oligonucleotides representative for a selective number of Methylococcus
PT   capsulatus genes -
XX
PS   Claim 14; Page 296-297; 678pp; English.
XX
CC   The invention relates to a novel DNA array giving a representation of a
CC   number of Methylococcus capsulatus genes. The method of the invention is
CC   useful for determination of the differential expression of the genes of
CC   M. capsulatus, and for studying gene expression on a genomic scale and in
CC   gene expression assays of M. capsulatus genes. The sequences shown in
CC   ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the
CC   invention.
XX
SQ   Sequence 2907 BP; 504 A; 975 C; 887 G; 541 T; 0 other;

  Query Match             36.3%;  Score 27.6;  DB 24;  Length 2907;
  Best Local Similarity   60.8%;  Pred. No. 21;
  Matches   45;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy       3 GTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGA 62
           ||||| || || ||||    | ||| || | | | | | | ||  ||| ||||||   ||
Db     915 GTTCAACATGATCGCCCACAATGGCGACATGGACGGCGTCTACCTCGAGTTCACCGTGGA 974

Qy      63 GGTGGTCAAGCCCC 76
             |  |  || | ||
Db     975 CGGCGAGAAACGCC 988


RESULT 40
AAZ25727
ID   AAZ25727 standard; cDNA; 1791 BP.
XX
AC   AAZ25727;
XX
DT   05-JAN-2000  (first entry)
XX
DE   Stachybotrys chartarum phenol oxidising enzyme encoding cDNA.
XX
KW   Stachybotrys chartarum; phenol oxidising enzyme; colour; dye;
KW   detergent; anti-dye transfer; stain removal; bleaching; ss.
XX
OS   Stachybotrys chartarum.
XX
PN   WO9949010-A2.
XX
PD   30-SEP-1999.
XX
PF   23-MAR-1999;   99WO-EP02042.
XX
PR   24-MAR-1998;   98US-0046969.
PR   22-DEC-1998;   98US-0218702.
XX
PA   (UNIL ) UNILEVER NV.
PA   (UNIL ) UNILEVER PLC.
XX
PI   Convents D,  Amory A,  Wang H,  Dhaese P,  Lambrechts-Rongvaux A;
PI   Wang C;
XX
DR   WPI; 1999-601211/51.
DR   P-PSDB; AAY45222.
XX
PT   Detergent composition containing phenol oxidase from Stachybotrys, used
PT   to bleach stains and prevent dye transfer -
XX
PS   Example 15; Fig 5; 56pp; English.
XX
CC   The present invention describes a detergent composition containing a
CC   purified phenol oxidising enzyme derived from Stachybotrys. The present
CC   sequence encodes Stachybotrys chartarum phenol oxidising enzyme. The
CC   enzyme can be used to modify the colour of dyes and other coloured
```

```
CC   compounds (e.g. for use in pulp and paper bleaching also for removing
CC   stains, e.g. food, tea, blood etc., from fabrics) and for preventing dye
CC   transfer during fabric washing.
XX
SQ   Sequence 1791 BP; 380 A; 554 C; 448 G; 409 T; 0 other;

  Query Match             36.1%;  Score 27.4;  DB 20;  Length 1791;
  Best Local Similarity   62.3%;  Pred. No. 23;
  Matches   43;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy       4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           ||||| ||||| || |   | | | ||||||| |  |  | |||| || | | |  |||
Db     577 TTCATGAAGACTGCTGAGAATGCCTACTTTGGTCAGGCTGGCGCCTACATTATCAACGAC 636

Qy      64 GTGGTCAAG 72
           | ||   ||
Db     637 GAGGCTGAG 645


RESULT 41
AAZ27601
ID   AAZ27601 standard; DNA; 1791 BP.
XX
AC   AAZ27601;
XX
DT   16-DEC-1999  (first entry)
XX
DE   Stachybotrys phenol oxidase coding sequence.
XX
KW   Phenol oxidase; enzyme; coloured compound; dye transfer prevention;
KW   fabric washing; stain bleaching; anti-dye transfer; detergent; ss.
XX
OS   Stachybotrys chartarum.
XX
PN   WO9949020-A2.
XX
PD   30-SEP-1999.
XX
PF   23-MAR-1999;   99WO-US06327.
XX
PR   24-MAR-1998;   98US-0046969.
PR   22-DEC-1998;   98US-0218702.
PR   22-MAR-1999;   99US-0273957.
XX
PA   (GEMV ) GENENCOR INT INC.
XX
PI   Amory A,  Wang H,  Dhase P,  Lambrechts-Rongvaux A,  Wang C;
XX
DR   WPI; 1999-591088/50.
DR   P-PSDB; AAY39992.
XX
PT   Novel enzyme for modifying coloured compounds used to prevent
PT   dye-transfer -
XX
PS   Claim 21; Fig 5; 64pp; English.
XX
CC   This sequence encodes the Stachybotrys chartarum phenol oxidase enzyme
CC   of the invention. The invention is used to modify a coloured compound and
CC   prevent dye transfer during fabric washing, or for stain bleaching or
CC   anti-dye transfer. It is useful in the detergent, paper and pulp, textile
CC   and food industries.
XX
SQ   Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other;

  Query Match             36.1%;  Score 27.4;  DB 20;  Length 1791;
  Best Local Similarity   62.3%;  Pred. No. 23;
  Matches   43;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy       4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           ||||| ||||| || |   | | | ||||||| |  |  | |||| || | | |  |||
Db     577 TTCATGAAGACTGCTGAGAATGCCTACTTTGGTCAGGCTGGCGCCTACATTATCAACGAC 636

Qy      64 GTGGTCAAG 72
           | ||   ||
Db     637 GAGGCTGAG 645


RESULT 42
AAA50019
ID   AAA50019 standard; DNA; 1791 BP.
XX
AC   AAA50019;
XX
DT   10-OCT-2000  (first entry)
XX
DE   Stachybotrys chartarum phenol oxidising enzyme cDNA.
XX
KW   Phenol oxidising enzyme; detergent; bleaching; ss.
XX
OS   Stachybotrys chartarum.
XX
FH   Key             Location/Qualifiers
FT   CDS             7..1791
FT                   /*tag=  a
XX
PN   WO200039306-A2.
XX
PD   06-JUL-2000.
XX
PF   20-DEC-1999;   99WO-EP10287.
XX
PR   23-DEC-1998;   98US-0220871.
PR   23-JUN-1999;   99US-0338723.
XX
PA   (UNIL ) UNILEVER NV.
PA   (UNIL ) UNILEVER PLC.
PA   (HIND-) HINDUSTAN LEVER LTD.
XX
PI   Bodie EA,  Van Der Velden S,  De Vries CH,  Wang H;
XX
DR   WPI; 2000-514528/46.
DR   P-PSDB; AAY95537.
XX
PT   Detergent composition comprising novel phenol oxidising enzyme obtained
PT   from fungus or bacteria, useful for pulp and paper bleaching, bleaching
PT   color of stains on fabric and for anti-dye redeposition -
XX
PS   Disclosure; Fig 5A-B; 45pp; English.
XX
CC   The present sequence is that of the Stachybotrys chartarum MUCL 38898
CC   cDNA encoding a phenol oxidising enzyme (see AAY95537). The invention
CC   relates to detergent compositions comprising novel phenol oxidising
CC   enzymes that are encoded by nucleic acids capable of hybridising to
CC   the S. chartarum phenol oxidising enzyme gene (see AAA50018), provided
CC   the enzymes are capable of modifying the colour associated with dyes
CC   or coloured compounds, and are produced from a bacterium, yeast or
CC   fungus (see AAY95538-40). The phenol oxidising enzymes can be used
CC   for pulp and paper bleaching, for bleaching the colour of stains on
CC   fabric and for anti-dye transfer in detergent and textile
CC   applications. They may also be capable of modifying the colour in
CC   the absence or presence of an enhancer. Expression vectors and host
CC   cells comprising a nucleic acid encoding a phenol oxidising enzyme,
CC   methods for producing the phenol oxidising enzyme, and methods for
CC   constructing expression hosts are provided.
XX
SQ   Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other;

  Query Match             36.1%;  Score 27.4;  DB 21;  Length 1791;
  Best Local Similarity   62.3%;  Pred. No. 23;
  Matches   43;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy       4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           ||||| ||||| || |   | | | ||||||| |  |  | |||| || | | |  |||
Db     577 TTCATGAAGACTGCTGAGAATGCCTACTTTGGTCAGGCTGGCGCCTACATTATCAACGAC 636

Qy      64 GTGGTCAAG 72
```

```
          | ||   ||
Db    637 GAGGCTGAG 645


RESULT 43
AAA51314
ID   AAA51314 standard; DNA; 1791 BP.
XX
AC   AAA51314;
XX
DT   09-OCT-2000  (first entry)
XX
DE   Stachybotrys chartarum phenol oxidizing enzyme cDNA.
XX
KW   Phenol oxidizing enzyme; colour; dye; modification; detergent; stain;
KW   pulp; paper bleaching; ss.
XX
OS   Stachybotrys chartarum.
XX
FH   Key             Location/Qualifiers
FT   CDS             7..1791
FT                   /*tag=  a
FT                   /product= Phenol_Oxidizing_Enzyme
XX
PN   WO200037654-A2.
XX
PD   29-JUN-2000.
XX
PF   20-DEC-1999;   99WO-US31009.
XX
PR   23-DEC-1998;   98US-0220871.
PR   23-JUN-1999;   99US-0338723.
XX
PA   (GEMV ) GENENCOR INT INC.
XX
PI   Wang H,  Bodie EA;
XX
DR   WPI; 2000-452191/39.
DR   P-PSDB; AAY96761.
XX
PT   New phenol oxidizing enzyme for modifying colors associated with dyes
PT   or colored compounds, is obtained from fungus and is encoded by a
PT   nucleic acid comprising a specific nucleotide sequence
XX
PS   Disclosure; Fig 5A-B; 45pp; English.
XX
CC   This cDNA encodes Stachybotrys chartarum phenol oxidizing enzyme.
CC   Phenol oxidizing enzymes encoded by nucleic acid sequences which
CC   hybridize to this DNA are claimed, as long as the enzyme is capable of
CC   modifying the colour associated with dyes or coloured compounds. The
CC   enzymes are useful in detergent compositions and for modifying colors
CC   associated with dyes or colored compounds which occur in stains in a
CC   sample. The enzymes are also useful for pulp and paper bleaching,
CC   anti-dye transfer in detergent and other textile applications.
XX
SQ   Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other;

  Query Match             36.1%;  Score 27.4;  DB 21;  Length 1791;
  Best Local Similarity   62.3%;  Pred. No. 23;
  Matches   43;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy       4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           ||||| ||||| || |   | | | |||||||  |  |  | |||| || | | |  |||
Db     577 TTCATGAAGACTGCTGAGAATGCCTACTTTGGTCAGGCTGGCGCCTACATTATCAACGAC 636

Qy      64 GTGGTCAAG 72
           | ||   ||
Db     637 GAGGCTGAG 645


RESULT 44
AAL47584
ID   AAL47584 standard; cDNA; 1791 BP.
XX
AC   AAL47584;
XX
DT   13-SEP-2002  (first entry)
XX
DE   S chartarum phenol oxidising enzyme cDNA.
XX
KW   Phenol oxidising enzyme; enzyme; fungus; redox reaction; detergent;
KW   paper industry; pulp industry; textile; food industry; gene; ss.
XX
OS   Stachybotrys chartarum.
XX
FH   Key             Location/Qualifiers
FT   CDS             7..1791
FT                   /*tag=  a
FT                   /product= "phenol oxidising enzyme"
XX
PN   US6399329-B1.
XX
PD   04-JUN-2002.
XX
PF   21-DEC-1999;   99US-0468578.
XX
PR   12-DEC-1998;   98US-0220871.
PR   23-JUN-1999;   99US-0338723.
XX
PA   (GEMV ) GENENCOR INT INC.
XX
PI   Wang H,  Bodie EA;
XX
DR   WPI; 2002-498835/53.
DR   P-PSDB; AAO18210.
XX
PT   New polynucleotides encoding phenol oxidizing enzymes, useful for
PT   preventing the transfer of dyes in solution from one textile to another
PT   during detergent washing -
XX
PS   Disclosure; Fig 5; 37pp; English.
XX
CC   The present invention provides the protein and coding sequences of phenol
CC   oxidising enzymes from Stachybotrys chartarum, Bipolaris spicifera and
CC   Curvularia pallescens. These enzymes are useful in the textiles, paper,
CC   pulp, detergent and food industries. In particular they are useful for
CC   preventing the transfer of dyes in solution from one textile to another
CC   during detergent washing (dye transfer inhibition). The present sequence
CC   is the S. chartarum phenol oxidising enzyme cDNA.
XX
SQ   Sequence 1791 BP; 380 A; 551 C; 451 G; 409 T; 0 other;

  Query Match             36.1%;  Score 27.4;  DB 24;  Length 1791;
  Best Local Similarity   62.3%;  Pred. No. 23;
  Matches   43;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy       4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           ||||| ||||| || |   | | | |||||||  |  |  | |||| || | | |  |||
Db     577 TTCATGAAGACTGCTGAGAATGCCTACTTTGGTCAGGCTGGCGCCTACATTATCAACGAC 636

Qy      64 GTGGTCAAG 72
           | ||   ||
Db     637 GAGGCTGAG 645


RESULT 45
ABA92911
ID   ABA92911 standard; DNA; 7248 BP.
XX
AC   ABA92911;
XX
DT   09-APR-2002  (first entry)
XX
DE   Stachybotrys chartarum laccase gene.
XX
KW   Laccase; enzyme; blue copper oxidase; fungal; oxidation; reduction;
```

KW copper; metal cofactor; gene; plant; ds.
XX
OS Stachybotrys chartarum.
XX
PN WO200196543-A2.
XX
PD 20-DEC-2001.
XX
PF 14-JUN-2001; 2001WO-US19174.
XX
PR 15-JUN-2000; 2000US-211732P.
XX
PA (PROD-) PRODIGENE INC.
PA (GEMV) GENENCOR INC.
XX
PI Hood E, Howard JA, Bailey M, Van Gastel FJC, Ward M, Wang H;
PI Woodard S;
XX
DR WPI; 2002-090204/12.
XX
PT Improving recovery of active enzyme e.g. laccase, which requires
PT transitional metal cofactor e.g. copper for activity, from a plant, by
PT introducing plant nucleotide sequences encoding the enzyme and exposing
PT it to cofactor -
XX
PS Example 5; Fig 16A-E; 81pp; English.
XX
CC The present invention describes a method for improving the recovery of
CC an active enzyme from a plant where the enzyme requires a transitional
CC metal cofactor for activity. The method comprises introducing into the
CC plant nucleotide sequences encoding the enzyme and exposing the enzyme
CC to the metal cofactor. The method is useful for improving recovery of
CC active enzyme which requires a transitional metal cofactor for activity,
CC preferably for improving recovery of active laccase which requires
CC copper for activity. The method can be used for improving recovery of
CC active organophosphate hydrolase (OPH, E.C. 3.1.8.1) which requires
CC zinc, nickel, cobalt or manganese for activity, where the method further
CC comprises adding bicarbonate ion salt. The present sequence encodes the
CC fungal Stachybotrys chartarum laccase enzyme. Laccases are also called
CC blue copper oxidases and use copper to accept and donate electrons in
CC the oxidation and reduction of substrates.
XX
SQ Sequence 7248 BP; 1928 A; 1744 C; 1579 G; 1997 T; 0 other;

Query Match 36.1%; Score 27.4; DB 24; Length 7248;
Best Local Similarity 62.3%; Pred. No. 26;
Matches 43; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

```
Qy       4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           ||||| ||||| || |   | | | ||||||| |  |  | |||| || | | |  |||
Db    5768 TTCATGAAGACTGCTGAGAATGCCTACTTTGGTCAGGCTGGCGCCTACATTATCAACGAC 5827

Qy      64 GTGGTCAAG 72
           | ||   ||
Db    5828 GAGGCTGAG 5836
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Search completed: April 23, 2003, 15:42:04
Job time : 2439.94 secs

GenCore version 5.1.4_p5_4578

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 23, 2003, 12:06:28 ; Search time 6.33333 Seconds
(without alignments)
2307.226 Million cell updates/sec

Title: US-09-198-779B-1_COPY_160_235
Perfect score: 138
Sequence: 1 aggttcatcaagaccgccgc.....ctgcgaggtggtcaagcccc 76

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09198779/runat_23042003_120617_2416/app_query.fasta_1.917
-DB=PIR_73 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=50
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=45 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09198779_@CGN_1_1_92_@runat_23042003_120617_2416 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	127	92.0	394	2	T06180	methionine adenosy
2	120	87.0	68	2	PQ0817	methionine adenosy
3	120	87.0	393	2	JN0131	methionine adenosy
4	120	87.0	393	2	S38875	methionine adenosy
5	120	87.0	393	2	S46538	methionine adenosy
6	120	87.0	393	2	C86155	S-adenosylmethioni
7	116	84.1	360	2	T06592	methionine adenosy
8	116	84.1	366	2	S66351	methionine adenosy
9	115	83.3	390	2	G84785	probable s-adenosy
10	115	83.3	393	2	JQ0410	methionine adenosy
11	108.5	78.6	397	2	S66352	methionine adenosy
12	101	73.2	179	2	T07899	methionine adenosy
13	101	73.2	390	2	S49491	methionine adenosy
14	101	73.2	390	2	S46540	methionine adenosy
15	98	71.0	396	2	T10710	methionine adenosy
16	74	53.6	395	2	G72228	S-adenosylmethioni
17	72	52.2	389	2	E81986	probable methionin
18	72	52.2	389	2	D81042	S-adenosylmethioni
19	68	49.3	388	2	S51671	methionine adenosy
20	65	47.1	400	2	D69657	methionine adenosy
21	64	46.4	376	2	A82895	S-adenosylmethioni
22	63	45.7	395	1	S27257	methionine adenosy
23	63	45.7	395	2	A37118	methionine adenosy
24	63	45.7	403	2	H86976	probable S-adenosy
25	61	44.2	376	2	F90599	hypothetical prote
26	61	44.2	385	2	D71964	s-adenosylmethioni
27	61	44.2	385	2	E64544	methionine adenosy
28	61	44.2	398	2	F89964	S-adenosylmethioni
29	61	44.2	399	2	D84062	S-adenosylmethioni
30	61	44.2	399	2	F86862	methionine adenosy
31	61	44.2	399	2	AD1654	S-methionine adeno
32	61	44.2	399	2	AH1282	S-methionine adeno
33	61	44.2	403	2	F70899	probable metK prot
34	61	44.2	420	2	B97403	methionine adenosy
35	61	44.2	420	2	AB2621	S-adenosylmethioni
36	60.5	43.8	409	2	S74736	methionine adenosy
37	60	43.5	385	2	E82319	S-adenosylmethioni
38	59	42.8	396	2	A71281	probable S-adenosy
39	59	42.8	396	2	A47151	methionine adenosy
40	59	42.8	397	2	S06114	methionine adenosy
41	58.5	42.4	238	2	H70866	hypothetical prote
42	58	42.0	378	2	E84977	methionine adenosy
43	58	42.0	1861	2	T13845	microtubule-associ
44	57	41.3	394	2	AE2211	S-adenosylmethioni
45	57	41.3	447	2	T50705	gamma-aminobutyrat
46	57	41.3	595	2	S72537	acr-2 protein - Ne
47	56	40.6	395	1	S27363	methionine adenosy
48	55.5	40.2	366	1	SAVLBD	large surface anti
49	55.5	40.2	407	2	B87255	S-adenosylmethioni
c 50	55	42.3	201	2	A82961	cytochrome c4 prec

ALIGNMENTS

RESULT 1
T06180
methionine adenosyltransferase (EC 2.5.1.6) - barley
N;Alternate names: S-adenosylmethionine synthetase
C;Species: Hordeum vulgare (barley)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 20-Jun-2000
C;Accession: T06180
R;Mori, S.
submitted to the EMBL Data Library, August 1995
A;Reference number: Z15512
A;Accession: T06180
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-394 <MOR>
A;Cross-references: EMBL:D63835; PIDN:BAA09895.1
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	1.16e-10	Length:	394
Score:	127.00	Matches:	24
Percent Similarity:	96.00%	Conservative:	0
Best Local Similarity:	96.00%	Mismatches:	1
Query Match:	92.03%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x T06180 (1-394)

```
Qy     1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   362 ArgPheIleLysThrAlaAlaTyrGlyHisPheGlyArgAspAspAlaAspPheThrTrp 381

Qy      61 GAGGTGGTCAAGCCC 75
```

```
          ||||||||||||||||
Db    382 GluValValLysPro 386

RESULT 2
PQ0817
methionine adenosyltransferase (EC 2.5.1.6) - rape (fragment)
C;Species: Brassica napus (rape)
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 05-May-2000
C;Accession: PQ0817
R;Park, Y.S.; Kwak, J.M.; Kwon, O.Y.; Kim, Y.S.; Lee, D.S.; Cho, M.J.; Lee, H.H.; Nam, H
Plant Physiol. 103, 359-370, 1993
A;Title: Generation of expressed sequence tags of random root cDNA clones of Brassica na
A;Reference number: PQ0816; MUID:94302145; PMID:8029332
A;Accession: PQ0817
A;Molecule type: mRNA
A;Residues: 1-68 <PAR>
A;Experimental source: root, cv. Naehan
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:              1.31e-09        Length:         68
Score:                  120.00          Matches:        22
Percent Similarity:     92.00%          Conservative:   1
Best Local Similarity:  88.00%          Mismatches:     2
Query Match:            86.96%          Indels:         0
DB:                     2               Gaps:           0

US-09-198-779B-1_COPY_160_235 (1-76) x PQ0817 (1-68)

Qy       1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
           ||||||:::|||||||||||||||||||||||||||||||||||||||   |||||||||
Db      36 ArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrp 55

Qy      61 GAGGTGGTCAAGCCC 75
           |||||||||||||||
Db      56 GluValValLysPro 60

RESULT 3
JN0131
methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana
N;Alternate names: S-adenosylmethionine synthetase
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 05-May-2000
C;Accession: JN0131
R;Peleman, J.; Boerjan, W.; Engler, G.; Seurinck, J.; Botterman, J.; Alliotte, T.; Van M
Plant Cell 1, 81-93, 1989
A;Title: Strong cellular preference in the expression of a housekeeping gene of Arabidop
A;Reference number: JN0131; MUID:92386056; PMID:2535470
A;Accession: JN0131
A;Molecule type: DNA
A;Residues: 1-393 <PEL>
A;Cross-references: GB:M55077; NID:g166871; PIDN:AAA32868.1; PID:g166872
A;Experimental source: var. K85
A;Note: the sequence derived from var. Columbia differs from that shown in having 117-Gl
A;Note: the authors translated the codon GAC for residue 117 as Glu
C;Comment: S-Adenosylmethionine synthetase catalyzes the biosysnthesis of adenosylmethic
C;Genetics:
A;Gene: sam-1
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:              1.31e-09        Length:         393
Score:                  120.00          Matches:        22
Percent Similarity:     92.00%          Conservative:   1
Best Local Similarity:  88.00%          Mismatches:     2
Query Match:            86.96%          Indels:         0
DB:                     2               Gaps:           0

US-09-198-779B-1_COPY_160_235 (1-76) x JN0131 (1-393)

Qy       1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
           ||||||:::|||||||||||||||||||||||||||||||||||||||   |||||||||
Db     361 ArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrp 380

Qy      61 GAGGTGGTCAAGCCC 75
           |||||||||||||||
Db     381 GluValValLysPro 385

RESULT 4
S38875
methionine adenosyltransferase (EC 2.5.1.6) - tomato
N;Alternate names: S-adenosyl-L-methionine synthetase
C;Species: Lycopersicon esculentum (tomato)
C;Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
C;Accession: S46539; S38875
R;Espartero, J.; Pintor-Toro, J.A.; Pardo, J.M.
Plant Mol. Biol. 25, 217-227, 1994
A;Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in
A;Reference number: S46538; MUID:94289646; PMID:8018871
A;Accession: S46539
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-393 <ES2>
A;Cross-references: EMBL:Z24742; NID:g429105; PIDN:CAA80866.1; PID:g429106
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:              1.31e-09        Length:         393
Score:                  120.00          Matches:        22
Percent Similarity:     92.00%          Conservative:   1
Best Local Similarity:  88.00%          Mismatches:     2
Query Match:            86.96%          Indels:         0
DB:                     2               Gaps:           0

US-09-198-779B-1_COPY_160_235 (1-76) x S38875 (1-393)

Qy       1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
           ||||||:::|||||||||||||||||||||||||||||||||||||||   |||||||||
Db     361 ArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrp 380

Qy      61 GAGGTGGTCAAGCCC 75
           |||||||||||||||
Db     381 GluValValLysPro 385

RESULT 5
S46538
methionine adenosyltransferase (EC 2.5.1.6) - tomato
N;Alternate names: S-adenosyl-L-methionine synthetase
C;Species: Lycopersicon esculentum (tomato)
C;Date: 26-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
C;Accession: S46538; S38874
R;Espartero, J.; Pintor-Toro, J.A.; Pardo, J.M.
Plant Mol. Biol. 25, 217-227, 1994
A;Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in
A;Reference number: S46538; MUID:94289646; PMID:8018871
A;Accession: S46538
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-393 <ESP>
A;Cross-references: EMBL:Z24741; NID:g429103; PIDN:CAA80865.1; PID:g429104
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:              1.31e-09        Length:         393
Score:                  120.00          Matches:        22
Percent Similarity:     92.00%          Conservative:   1
Best Local Similarity:  88.00%          Mismatches:     2
Query Match:            86.96%          Indels:         0
DB:                     2               Gaps:           0

US-09-198-779B-1_COPY_160_235 (1-76) x S46538 (1-393)
```

```
Qy       1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
           ||||||:::||||||||||||||||||||||||||||||||||||   |||||||||
Db     361 ArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrp 380

Qy      61 GAGGTGGTCAAGCCC 75
           |||||||||||||||
Db     381 GluValValLysPro 385
```

RESULT 6
C86155
S-adenosylmethionine synthetase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C86155
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C86155
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-393 <STO>
A;Cross-references: GB:AE005172; NID:g9972389; PIDN:AAG10639.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	1.31e-09	Length:	393
Score:	120.00	Matches:	22
Percent Similarity:	92.00%	Conservative:	1
Best Local Similarity:	88.00%	Mismatches:	2
Query Match:	86.96%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x C86155 (1-393)

```
Qy       1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
           ||||||:::||||||||||||||||||||||||||||||||||||   |||||||||
Db     361 ArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrp 380

Qy      61 GAGGTGGTCAAGCCC 75
           |||||||||||||||
Db     381 GluValValLysPro 385
```

RESULT 7
T06592
methionine adenosyltransferase (EC 2.5.1.6) - garden pea (fragment)
C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C;Accession: T06592
R;Gomez, L.; Carrasco, P.
submitted to the EMBL Data Library, January 1995
A;Description: Hormonal regulation of the S-adenosylmethionine synthase in pea ovaries.
A;Reference number: Z15782
A;Accession: T06592
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-360 <GOM>
A;Cross-references: EMBL:L36680; NID:g609556; PIDN:AAA58772.1; PID:g609557
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	5.23e-09	Length:	360
Score:	116.00	Matches:	21
Percent Similarity:	92.00%	Conservative:	2
Best Local Similarity:	84.00%	Mismatches:	2
Query Match:	84.06%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x T06592 (1-360)

```
Qy       1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
           ||||||:::|||||||||||||||||||||||||||||||:::|||   |||||||||
Db     330 ArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrp 349

Qy      61 GAGGTGGTCAAGCCC 75
           |||||||||||||||
Db     350 GluValValLysPro 354
```

RESULT 8
S66351
methionine adenosyltransferase (EC 2.5.1.6) 1 - garden pea (fragment)
C;Species: Pisum sativum (garden pea)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-May-2000
C;Accession: S66351
R;Gomez-Gomez, L.; Carrasco, P.
Plant Mol. Biol. 30, 821-832, 1996
A;Title: Hormonal regulation of S-adenosylmethionine synthase transcripts in pea ovar
A;Reference number: S66351; MUID:96194463; PMID:8624412
A;Accession: S66351
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-366 <GOM>
A;Cross-references: EMBL:X82076; NID:g609222; PIDN:CAA57580.1; PID:g609223
A;Note: the authors did not translate the codon for residue 1
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	5.22e-09	Length:	366
Score:	116.00	Matches:	21
Percent Similarity:	92.00%	Conservative:	2
Best Local Similarity:	84.00%	Mismatches:	2
Query Match:	84.06%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x S66351 (1-366)

```
Qy       1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
           ||||||:::|||||||||||||||||||||||||||||||:::|||   |||||||||
Db     336 ArgPheLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrp 355

Qy      61 GAGGTGGTCAAGCCC 75
           |||||||||||||||
Db     356 GluValValLysPro 360
```

RESULT 9
G84785
probable s-adenosylmethionine synthetase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: G84785
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84785
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-390 <STO>
A;Cross-references: GB:AE002093; NID:g4883604; PIDN:AAD31573.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g36880
A;Map position: 2
C;Superfamily: methionine adenosyltransferase

```
Alignment Scores:
Pred. No.:                7.38e-09        Length:         390
Score:                    115.00          Matches:        22
Percent Similarity:       88.00%          Conservative:   0
Best Local Similarity:    88.00%          Mismatches:     3
Query Match:              83.33%          Indels:         0
DB:                       2               Gaps:           0

US-09-198-779B-1_COPY_160_235 (1-76) x G84785 (1-390)

Qy       1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
           ||||||   ||||||||||||||||||||||||||||||||||||   |||||||||
Db     361 ArgPheGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrp 380

Qy      61 GAGGTGGTCAAGCCC 75
           |||||||||||||||
Db     381 GluValValLysPro 385

RESULT 10
JQ0410
methionine adenosyltransferase (EC 2.5.1.6) 2 - Arabidopsis thaliana
N;Alternate names: S-adenosylmethionine synthetase
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-May-2000
C;Accession: JQ0410
R;Peleman, J.; Saito, K.; Cottyn, B.; Engler, G.; Seurinck, J.; Van Montagu, M.; Inze, D
Gene 84, 359-369, 1989
A;Title: Structure and expression analyses of the S-adenosylmethionine synthetase gene f
A;Reference number: JQ0410; MUID:90128280; PMID:2482229
A;Accession: JQ0410
A;Molecule type: DNA
A;Residues: 1-393 <PEL>
A;Cross-references: GB:M33217; NID:g166873; PIDN:AAA32869.1; PID:g166874
C;Genetics:
A;Gene: sam-2
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:                7.38e-09        Length:         393
Score:                    115.00          Matches:        22
Percent Similarity:       88.00%          Conservative:   0
Best Local Similarity:    88.00%          Mismatches:     3
Query Match:              83.33%          Indels:         0
DB:                       2               Gaps:           0

US-09-198-779B-1_COPY_160_235 (1-76) x JQ0410 (1-393)

Qy       1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
           ||||||   ||||||||||||||||||||||||||||||||||||   |||||||||
Db     361 ArgPheGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrp 380

Qy      61 GAGGTGGTCAAGCCC 75
           |||||||||||||||
Db     381 GluValValLysPro 385

RESULT 11
S66352
methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-May-2000
C;Accession: S66352; S52218
R;Gomez-Gomez, L.; Carrasco, P.
Plant Mol. Biol. 30, 821-832, 1996
A;Title: Hormonal regulation of S-adenosylmethionine synthase transcripts in pea ovaries
A;Reference number: S66351; MUID:96194463; PMID:8624412
A;Accession: S66352
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-397 <GOM>
A;Cross-references: EMBL:X82077
R;Gomez, L.; Carrasco, P.
submitted to the EMBL Data Library, October 1994
A;Description: Hormonal regulation of the s-adenosylmethionine synthase in pea ovarie
A;Reference number: S52218
A;Accession: S52218
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-364,'FEDSCIWTFW' <GOW>
A;Cross-references: EMBL:X82077; NID:g609224; PIDN:CAA57581.1; PID:g609225
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:                7e-08           Length:         397
Score:                    108.50          Matches:        22
Percent Similarity:       88.46%          Conservative:   1
Best Local Similarity:    84.62%          Mismatches:     2
Query Match:              78.62%          Indels:         1
DB:                       2               Gaps:           1

US-09-198-779B-1_COPY_160_235 (1-76) x S66352 (1-397)

Qy       1 AGGTTC---ATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACC 57
           ||||||   :::||||||||||||||||||||||||||   ||||||||||||||||||
Db     363 ArgPheLeuLeuLysThrAlaAlaTyrGlyHisPheGlySerAspAspAlaAspPheThr 382

Qy      58 TGCGAGGTGGTCAAGCCC 75
              ||||||||||||||||
Db     383 TrpGluValValLysPro 388

RESULT 12
T07899
methionine adenosyltransferase (EC 2.5.1.6) - Chlamydomonas reinhardtii (fragment)
N;Alternate names: S-adenosylmethionine synthetase
C;Species: Chlamydomonas reinhardtii
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 05-May-2000
C;Accession: T07899
R;Kim, J.Y.; Lee, K.O.; Lee, S.H.
submitted to the EMBL Data Library, June 1997
A;Description: Chlamydomonas reinhardtii mRNA for S-adenosylmethionine synthetase.
A;Reference number: Z16198
A;Accession: T07899
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-179 <KIM>
A;Cross-references: EMBL:AF008568; NID:g2454483; PIDN:AAB71833.1; PID:g2454484
A;Experimental source: strain 137C
C;Genetics:
A;Gene: SAMS
C;Function:
A;Description: catalyzes the formation of S-adenosyl methionine with phosphate and py
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:                9.4e-07         Length:         179
Score:                    101.00          Matches:        19
Percent Similarity:       83.33%          Conservative:   1
Best Local Similarity:    79.17%          Mismatches:     4
Query Match:              73.19%          Indels:         0
DB:                       2               Gaps:           0

US-09-198-779B-1_COPY_160_235 (1-76) x T07899 (1-179)

Qy       1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
           |||:::   ||||||||||||||||||||||||||||||||||||   |||||||||
Db     153 ArgTyrGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrp 172

Qy      61 GAGGTGGTCAAG 72
           |||   ||||||
Db     173 GluThrValLys 176

RESULT 13
S49491
```

methionine adenosyltransferase (EC 2.5.1.6) - garden petunia
C;Species: Petunia x hybrida (garden petunia)
C;Date: 01-Feb-1995 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
C;Accession: S49491
R;Izhaki, A.; Shoseyov, O.; Weiss, D.
submitted to the EMBL Data Library, October 1994
A;Description: Petunia cDNA encoding S-Adenosylmethionine synthetase.
A;Reference number: S49491
A;Accession: S49491
A;Molecule type: mRNA
A;Residues: 1-390 <IZH>
A;Cross-references: EMBL:X82214; NID:g559505; PIDN:CAA57696.1; PID:g559506
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	9.39e-07	Length:	390
Score:	101.00	Matches:	19
Percent Similarity:	83.33%	Conservative:	1
Best Local Similarity:	79.17%	Mismatches:	4
Query Match:	73.19%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x S49491 (1-390)

```
Qy      1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
          |||:::   ||||||||||||||||||||||||||||||||||||   |||||||||
Db    361 ArgTyrGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrp 380

Qy     61 GAGGTGGTCAAG 72
          |||   ||||||
Db    381 GluThrValLys 384
```

RESULT 14
S46540
methionine adenosyltransferase (EC 2.5.1.6) - tomato
N;Alternate names: S-adenosyl-L-methionine synthetase
C;Species: Lycopersicon esculentum (tomato)
C;Date: 26-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
C;Accession: S46540; S38876
R;Espartero, J.; Pintor-Toro, J.A.; Pardo, J.M.
Plant Mol. Biol. 25, 217-227, 1994
A;Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in res
A;Reference number: S46538; MUID:94289646; PMID:8018871
A;Accession: S46540
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-390 <ESP>
A;Cross-references: EMBL:Z24743; NID:g429107; PIDN:CAA80867.1; PID:g429108
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	9.39e-07	Length:	390
Score:	101.00	Matches:	19
Percent Similarity:	83.33%	Conservative:	1
Best Local Similarity:	79.17%	Mismatches:	4
Query Match:	73.19%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x S46540 (1-390)

```
Qy      1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
          |||:::   ||||||||||||||||||||||||||||||||||||   |||||||||
Db    361 ArgTyrGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAspPheThrTrp 380

Qy     61 GAGGTGGTCAAG 72
          |||   ||||||
Db    381 GluThrValLys 384
```

RESULT 15
T10710
methionine adenosyltransferase (EC 2.5.1.6) - clove pink
N;Alternate names: S-adenosylmethionine synthetase
C;Species: Dianthus caryophyllus (clove pink)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-May-2000
C;Accession: T10710
R;Larsen, P.B.; Woodson, W.R.
submitted to the EMBL Data Library, April 1991
A;Description: Cloning and nucleotide sequence of a s-adenosylmethionine synthetase c
A;Reference number: Z17091
A;Accession: T10710
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-396 <LAR>
A;Cross-references: EMBL:M61882; NID:g167961; PID:g304637
C;Genetics:
A;Gene: SAM2
C;Function:
A;Description: catalyzes the formation of S-adenosyl methionine with phosphate and py
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	2.65e-06	Length:	396
Score:	98.00	Matches:	17
Percent Similarity:	83.33%	Conservative:	3
Best Local Similarity:	70.83%	Mismatches:	4
Query Match:	71.01%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x T10710 (1-396)

```
Qy      1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
          |||::::::|||||||||||||||||||||||||||||||:::|||   |||||||||
Db    364 ArgTyrLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAspPheThrTrp 383

Qy     61 GAGGTGGTCAAG 72
          |||      |||
Db    384 GluAlaAlaLys 387
```

RESULT 16
G72228
S-adenosylmethionine synthetase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: G72228
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: G72228
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-395 <ARN>
A;Cross-references: GB:AE001807; GB:AE000512; NID:g4982216; PIDN:AAD36725.1; PID:g498
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1658
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	0.0107	Length:	395
Score:	74.00	Matches:	13
Percent Similarity:	88.89%	Conservative:	3
Best Local Similarity:	72.22%	Mismatches:	2
Query Match:	53.62%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x G72228 (1-395)

```
Qy     10 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
          |||||||||||||||||||||||||||||::::::   :::|||||||   |||
Db    364 LysThrAlaAlaTyrGlyHisPheGlyArgAsnGluGluGluPheThrTrpGlu 381
```

RESULT 17
E81986
probable methionine adenosyltransferase (EC 2.5.1.6) NMA0663 [imported] - Neisseria meni
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: E81986
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: E81986
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 <PAR>
A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83950.1; PID:g737939
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: metK; NMA0663
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	0.0214	Length:	389
Score:	72.00	Matches:	12
Percent Similarity:	85.00%	Conservative:	5
Best Local Similarity:	60.00%	Mismatches:	3
Query Match:	52.17%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x E81986 (1-389)

```
Qy       4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           :::   |||:::|||||||||||||||||||||||||||:::::   :::||||||   |||
Db     356 TyrSerLysSerAlaAlaTyrGlyHisPheGlyArgGluGluProGluPheThrTrpGlu 375
```

RESULT 18
D81042
S-adenosylmethionine synthetase NMB1799 [imported] - Neisseria meningitidis (strain MC58
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: D81042
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: D81042
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 <TET>
A;Cross-references: GB:AE002530; GB:AE002098; NID:g7227054; PIDN:AAF42136.1; PID:g722705
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1799
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	0.0214	Length:	389
Score:	72.00	Matches:	12
Percent Similarity:	85.00%	Conservative:	5
Best Local Similarity:	60.00%	Mismatches:	3
Query Match:	52.17%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x D81042 (1-389)

```
Qy       4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           :::   |||:::|||||||||||||||||||||||||||:::::   :::||||||   |||
Db     356 TyrSerLysSerAlaAlaTyrGlyHisPheGlyArgGluGluProGluPheThrTrpGlu 375
```

RESULT 19
S51671
methionine adenosyltransferase (EC 2.5.1.6) - Acanthamoeba castellanii
C;Species: Acanthamoeba castellanii
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 05-May-2000
C;Accession: S51671
R;Ahn, K.S.; Henney, H.
submitted to the EMBL Data Library, May 1994
A;Reference number: S51671
A;Accession: S51671
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-388 <AHN>
A;Cross-references: EMBL:X79205
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	0.0856	Length:	388
Score:	68.00	Matches:	13
Percent Similarity:	71.43%	Conservative:	2
Best Local Similarity:	61.90%	Mismatches:	6
Query Match:	49.28%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x S51671 (1-388)

```
Qy      10 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTC 69
           |||||||||   :::|||||||||||||||||:::|||   ||||||      |||
Db     364 LysThrAlaTyrHisGlyHisPheGlyArgAsnAspProAspPheLeuTrpGluAlaPro 383

Qy      70 AAG 72
           |||
Db     384 Lys 384
```

RESULT 20
D69657
methionine adenosyltransferase (EC 2.5.1.6) - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: D69657
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: D69657
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-400 <KUN>
A;Cross-references: GB:Z99119; GB:AL009126; NID:g2635411; PIDN:CAB15033.1; PID:g26355
A;Experimental source: strain 168
C;Genetics:
A;Gene: metK
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	0.242	Length:	400
Score:	65.00	Matches:	12
Percent Similarity:	72.22%	Conservative:	1

```
Best Local Similarity:  66.67%          Mismatches:     5
Query Match:            47.10%          Indels:         0
DB:                     2               Gaps:           0

US-09-198-779B-1_COPY_160_235 (1-76) x D69657 (1-400)

Qy      10 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           :::|||||||||||||||||||||||||||   |||  |||         |||
Db     368 GlnThrAlaAlaTyrGlyHisPheGlyArgHisAspValAspLeuProTrpGlu 385

RESULT 21
A82895
S-adenosylmethionine synthetase UU412 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: A82895
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A;Reference number: A82870
A;Accession: A82895
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <GLA>
A;Cross-references: GB:AE002138; GB:AF222894; NID:g6899390; PIDN:AAF30823.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: metK; UU412
A;Genetic code: SGC3
C;Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.:              0.342           Length:         376
Score:                  64.00           Matches:        10
Percent Similarity:     71.43%          Conservative:   5
Best Local Similarity:  47.62%          Mismatches:     6
Query Match:            46.38%          Indels:         0
DB:                     2               Gaps:           0

US-09-198-779B-1_COPY_160_235 (1-76) x A82895 (1-376)

Qy       1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
           :::::::::      |||   |||||||||||||||||||||||   :::   :::
Db     343 LysTyrLeuProValAlaThrTyrGlyHisPheGlyArgAspAspLeuAsnLeuSerTrp 362

Qy      61 GAG 63
           |||
Db     363 Glu 363

RESULT 22
S27257
methionine adenosyltransferase (EC 2.5.1.6) 2 alpha chain - human
N;Alternate names: renal methionine adenosyltransferase (MAT); S-adenosylmethionine synt
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 11-Jun-1999
C;Accession: S27257
R;Horikawa, S.; Tsukada, K.
FEBS Lett. 312, 37-41, 1992
A;Title: Molecular cloning and developmental expression of a human kidney S-adenosylmeth
A;Reference number: S27257; MUID:93050159; PMID:1426236
A;Accession: S27257
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-395 <HOR>
A;Cross-references: EMBL:X68836; GB:S47859; NID:g36326; PIDN:CAA48726.1; PID:g36327
C;Genetics:
A;Gene: GDB:MAT2A; SAMS2; MATA2
A;Cross-references: GDB:136213; OMIM:601468
A;Map position: 2p11.2-2p11.2
A;Introns: 15/2; 256/3
C;Complex: heterodimer of catalytic alpha and regulatory beta chains
C;Function:
A;Description: catalyzes the formation of S-adenosyl methionine with phosphate and pyrop
A;Pathway: one-carbon metabolism
C;Superfamily: methionine adenosyltransferase
C;Keywords: ATP; heterodimer; kidney; magnesium; metalloprotein; one-carbon metabolis
F;279-286/Region: nucleotide-binding motif A (P-loop) #status atypical
F;31/Binding site: magnesium 2 (Asp) #status predicted
F;285,289/Active site: Lys #status predicted
F;291/Binding site: magnesium 1 (Asp) #status predicted

Alignment Scores:
Pred. No.:              0.483           Length:         395
Score:                  63.00           Matches:        14
Percent Similarity:     71.43%          Conservative:   1
Best Local Similarity:  66.67%          Mismatches:     4
Query Match:            45.65%          Indels:         2
DB:                     1               Gaps:           1

US-09-198-779B-1_COPY_160_235 (1-76) x S27257 (1-395)

Qy      10 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTC 69
           :::|||||||||||||||||||||||||||||||         |||      ||||||
Db     373 ArgThrAlaAlaTyrGlyHisPheGlyArgAsp------SerPheProTrpGluValPro 390

Qy      70 AAG 72
           |||
Db     391 Lys 391

RESULT 23
A37118
methionine adenosyltransferase (EC 2.5.1.6) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 05-May-2000
C;Accession: A37118
R;Horikawa, S.; Sasuga, J.; Shimizu, K.; Ozasa, H.; Tsukada, K.
J. Biol. Chem. 265, 13683-13686, 1990
A;Title: Molecular cloning and nucleotide sequence of cDNA encoding the rat kidney S-
A;Reference number: A37118; MUID:90337979; PMID:1696256
A;Accession: A37118
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-395 <HOR>
A;Cross-references: GB:J05571; NID:g206845; PIDN:AAA42106.1; PID:g206846
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:              0.483           Length:         395
Score:                  63.00           Matches:        14
Percent Similarity:     71.43%          Conservative:   1
Best Local Similarity:  66.67%          Mismatches:     4
Query Match:            45.65%          Indels:         2
DB:                     2               Gaps:           1

US-09-198-779B-1_COPY_160_235 (1-76) x A37118 (1-395)

Qy      10 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTC 69
           :::|||||||||||||||||||||||||||||||         |||      ||||||
Db     373 ArgThrAlaAlaTyrGlyHisPheGlyArgAsp------SerPheProTrpGluValPro 390

Qy      70 AAG 72
           |||
Db     391 Lys 391

RESULT 24
H86976
probable S-adenosylmethionine synthase [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: H86976
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holro
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;
```

```
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: H86976
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-403 <STO>
A;Cross-references: GB:AL450380; NID:g13092748; PIDN:CAC30052.1; GSPDB:GN00147
C;Genetics:
A;Gene: metK
C;Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.:              0.483          Length:         403
Score:                  63.00          Matches:        11
Percent Similarity:     70.00%         Conservative:   3
Best Local Similarity:  55.00%         Mismatches:     6
Query Match:            45.65%         Indels:         0
DB:                     2              Gaps:           0

US-09-198-779B-1_COPY_160_235 (1-76) x H86976 (1-403)

Qy       4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           :::   :::|||||||||||||||||||||||||||||   |||   :::      |||
Db     372 TyrAlaGlnThrAlaAlaTyrGlyHisPheGlyArgThrAspValGluLeuProTrpGlu 391

RESULT 25
F90599
hypothetical protein MYPU_7020 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: F90599
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: F90599
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <KUR>
A;Cross-references: GB:AL445566; PID:g14090117; PIDN:CAC13875.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPU_7020
A;Genetic code: SGC3
C;Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.:              0.965          Length:         376
Score:                  61.00          Matches:        10
Percent Similarity:     66.67%         Conservative:   4
Best Local Similarity:  47.62%         Mismatches:     7
Query Match:            44.20%         Indels:         0
DB:                     2              Gaps:           0

US-09-198-779B-1_COPY_160_235 (1-76) x F90599 (1-376)

Qy       1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGC 60
           ::::::      |||:::   :::||||||||||||||||||||   |||
Db     343 LysTyrProThrSerPhePheGlyHisPheGlyArgAspAspLeuAspLeuProTrp 362

Qy      61 GAG 63
           |||
Db     363 Glu 363

RESULT 26
D71964
s-adenosylmethionine synthetase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 18-Jun-1999
C;Accession: D71964
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric p
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: D71964
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-385 <ARN>
A;Cross-references: GB:AE001456; GB:AE001439; NID:g4154689; PIDN:AAD05755.1; PID:g415
A;Experimental source: strain J99
C;Genetics:
A;Gene: metK
C;Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.:              0.965          Length:         385
Score:                  61.00          Matches:        11
Percent Similarity:     82.35%         Conservative:   3
Best Local Similarity:  64.71%         Mismatches:     3
Query Match:            44.20%         Indels:         0
DB:                     2              Gaps:           0

US-09-198-779B-1_COPY_160_235 (1-76) x D71964 (1-385)

Qy      13 ACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           |||:::|||||||||||||||||||||:::      :::||||||   |||
Db     355 ThrSerAlaTyrGlyHisPheGlyArgGluLeuGluGluPheThrTrpGlu 371

RESULT 27
E64544
methionine adenosyltransferase (EC 2.5.1.6) 2 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 05-May-2000
C;Accession: E64544
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKe
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: E64544
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-385 <TOM>
A;Cross-references: GB:AE000540; GB:AE000511; NID:g2313287; PIDN:AAD07267.1; PID:g231
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:              0.965          Length:         385
Score:                  61.00          Matches:        11
Percent Similarity:     82.35%         Conservative:   3
Best Local Similarity:  64.71%         Mismatches:     3
Query Match:            44.20%         Indels:         0
DB:                     2              Gaps:           0

US-09-198-779B-1_COPY_160_235 (1-76) x E64544 (1-385)

Qy      13 ACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           |||:::|||||||||||||||||||||:::      :::||||||   |||
Db     355 ThrSerAlaTyrGlyHisPheGlyArgGluLeuGluGluPheThrTrpGlu 371

RESULT 28
F89964
S-adenosylmethionine synthetase [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: F89964
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
```

A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: F89964
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-398 <KUR>
A;Cross-references: GB:BA000018; PID:g13701583; PIDN:BAB42876.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: metK
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	0.965	Length:	398
Score:	61.00	Matches:	12
Percent Similarity:	72.22%	Conservative:	1
Best Local Similarity:	66.67%	Mismatches:	5
Query Match:	44.20%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x F89964 (1-398)

```
Qy      10 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           :::|||||||||||||||||||||||||||   |||      |||      |||
Db     367 GlnThrAlaAlaTyrGlyHisPheGlyArgThrAspValLeuPheProTrpGlu 384
```

RESULT 29
D84062
S-adenosylmethionine synthetase metK [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: D84062
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D84062
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-399 <STO>
A;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB07019.1; GSPDB:GN0
A;Experimental source: strain C-125
C;Genetics:
A;Gene: metK
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	0.965	Length:	399
Score:	61.00	Matches:	11
Percent Similarity:	72.22%	Conservative:	2
Best Local Similarity:	61.11%	Mismatches:	5
Query Match:	44.20%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x D84062 (1-399)

```
Qy      10 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           :::|||||||||||||||||||||||||||   |||   :::         |||
Db     370 GlnThrAlaAlaTyrGlyHisPheGlyArgThrAspValGluLeuProTrpGlu 387
```

RESULT 30
F86862
methionine adenosyltransferase (EC 2.5.1.6) [imported] - Lactococcus lactis subsp. lacti
N;Alternate names: S-adenosylmethionine synthetase
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: F86862
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: F86862
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-399 <STO>
A;Cross-references: GB:AE005176; PID:g12724937; PIDN:AAK06000.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: metK
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	0.965	Length:	399
Score:	61.00	Matches:	11
Percent Similarity:	72.22%	Conservative:	2
Best Local Similarity:	61.11%	Mismatches:	5
Query Match:	44.20%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x F86862 (1-399)

```
Qy      10 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           :::|||||||||||||||||||||||||||   |||   :::         |||
Db     368 GlnThrAlaAlaTyrGlyHisPheGlyArgThrAspValGluLeuProTrpGlu 385
```

RESULT 31
AD1654
S-methionine adenosyltransferase homolog metK [imported] - Listeria innocua (strain C
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AD1654
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1654
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-399 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC97004.1; PID:g16414260; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: metK
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	0.965	Length:	399
Score:	61.00	Matches:	11
Percent Similarity:	72.22%	Conservative:	2
Best Local Similarity:	61.11%	Mismatches:	5
Query Match:	44.20%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x AD1654 (1-399)

```
Qy      10 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           :::|||||||||:::|||||||||||||||   |||   |||         |||
Db     368 GlnThrAlaAlaPheGlyHisPheGlyArgSerAspLeuAspLeuProTrpGlu 385
```

RESULT 32
AH1282
S-methionine adenosyltransferase homolog metK [imported] - Listeria monocytogenes (st
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AH1282
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1282
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-399 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC99742.1; PID:g16411100; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: metK
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	0.965	Length:	399
Score:	61.00	Matches:	11
Percent Similarity:	72.22%	Conservative:	2
Best Local Similarity:	61.11%	Mismatches:	5
Query Match:	44.20%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x AH1282 (1-399)

```
Qy      10 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           :::|||||||||:::|||||||||||||||   |||   |||         |||
Db     368 GlnThrAlaAlaPheGlyHisPheGlyArgSerAspLeuAspLeuProTrpGlu 385
```

RESULT 33
F70899
probable metK protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: F70899
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70899
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-403 <COL>
A;Cross-references: GB:Z80108; GB:AL123456; NID:g3256012; PIDN:CAB02194.1; PID:g3256013
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: metK
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	0.965	Length:	403
Score:	61.00	Matches:	11
Percent Similarity:	65.00%	Conservative:	2
Best Local Similarity:	55.00%	Mismatches:	7
Query Match:	44.20%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x F70899 (1-403)

```
Qy       4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAG 63
           :::      |||||||||||||||||||||||||||   |||   :::         |||
Db     372 TyrAlaProThrAlaAlaTyrGlyHisPheGlyArgThrAspValGluLeuProTrpGlu 391
```

RESULT 34
B97403
methionine adenosyltransferase (EC 2.5.1.6) - Agrobacterium tumefaciens (strain C58, Cer
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: B97403
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; PMID:11743194
A;Accession: B97403
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-420 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK86179.1; PID:g15155274; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C_632
A;Map position: circular chromosome
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:

Pred. No.:	0.965	Length:	420
Score:	61.00	Matches:	14
Percent Similarity:	63.33%	Conservative:	5
Best Local Similarity:	46.67%	Mismatches:	5
Query Match:	44.20%	Indels:	6
DB:	2	Gaps:	2

US-09-198-779B-1_COPY_160_235 (1-76) x B97403 (1-420)

```
Qy       4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGAC---------GACGCCGACTTC 54
           :::   ||||||::::::|||||||||||||||||||            |||     |||
Db     384 TyrAlaLysThrSerSerTyrGlyHisPheGlyArgLysAlaGlyArgAspGlySerPhe 403

Qy      55 ACCTGCGAG---------GTGGTCAAGCCC 75
           :::   |||         :::|||||||||
Db     404 SerTrpGluLysLeuAspLeuValLysPro 413
```

RESULT 35
AB2621
S-adenosylmethionine synthetase metK [imported] - Agrobacterium tumefaciens (strain C
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C;Accession: AB2621
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AB2621
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-420 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL41384.1; PID:g17738701; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: metK
A;Map position: circular chromosome
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	0.965	Length:	420
Score:	61.00	Matches:	14
Percent Similarity:	63.33%	Conservative:	5
Best Local Similarity:	46.67%	Mismatches:	5
Query Match:	44.20%	Indels:	6
DB:	2	Gaps:	2

US-09-198-779B-1_COPY_160_235 (1-76) x AB2621 (1-420)

```
Qy       4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGAC---------GACGCCGACTTC 54
           :::   ||||||::::::|||||||||||||||||||            |||     |||
Db     384 TyrAlaLysThrSerSerTyrGlyHisPheGlyArgLysAlaGlyArgAspGlySerPhe 403

Qy      55 ACCTGCGAG---------GTGGTCAAGCCC 75
           :::   |||         :::|||||||||
Db     404 SerTrpGluLysLeuAspLeuValLysPro 413
```

RESULT 36

```
S74736
methionine adenosyltransferase (EC 2.5.1.6) - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein sll0927; S-adenosylmethionine synthetase
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S74736
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74736
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-409 <KAN>
A;Cross-references: EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAA16887.1; PID:g165196
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: metX
A;Start codon: GTG
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:                1.15        Length:          409
Score:                    60.50       Matches:         13
Percent Similarity:       68.18%      Conservative:    2
Best Local Similarity:    59.09%      Mismatches:      6
Query Match:              43.84%      Indels:          1
DB:                       2           Gaps:            1

US-09-198-779B-1_COPY_160_235 (1-76) x S74736 (1-409)

Qy       1 AGGTTCATCAAG---ACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACC 57
           ||||||   :::     ||||||||||||||||||||||||:::|||   |||
Db     367 ArgPheTyrGlnAspValAlaAlaTyrGlyHisPheGlyArgAsnAspLeuAspLeuPro 386

Qy      58 TGCGAG 63
              |||
Db     387 TrpGlu 388

RESULT 37
E82319
S-adenosylmethionine synthase VC0472 [imported] - Vibrio cholerae (strain N16961 serogrc
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: E82319
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: E82319
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-385 <HEI>
A;Cross-references: GB:AE004133; GB:AE003852; NID:g9654889; PIDN:AAF93645.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0472
A;Map position: 1
C;Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.:                1.36        Length:          385
Score:                    60.00       Matches:         10
Percent Similarity:       100.00%     Conservative:    2
Best Local Similarity:    83.33%      Mismatches:      0
Query Match:              43.48%      Indels:          0
DB:                       2           Gaps:            0

US-09-198-779B-1_COPY_160_235 (1-76) x E82319 (1-385)

Qy      10 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGAC 45
           ||||||||||||||||||||||||||||||:::::
Db     355 LysThrAlaAlaTyrGlyHisPheGlyArgGluGlu 366

RESULT 38
A71281
probable S-adenosylmethionine synthetase (metK) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 18-Jun-1999
C;Accession: A71281
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; G
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; M
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: A71281
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-396 <COL>
A;Cross-references: GB:AE001250; GB:AE000520; NID:g3323096; PIDN:AAC65758.1; PID:g332
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0794
C;Superfamily: methionine adenosyltransferase

Alignment Scores:
Pred. No.:                1.93        Length:          396
Score:                    59.00       Matches:         13
Percent Similarity:       54.55%      Conservative:    5
Best Local Similarity:    39.39%      Mismatches:      7
Query Match:              42.75%      Indels:          8
DB:                       2           Gaps:            2

US-09-198-779B-1_COPY_160_235 (1-76) x A71281 (1-396)

Qy       1 AGGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGAC---------------- 45
           |||:::     ||||||  ||||||||||||||||||:::
Db     355 ArgTyrArgSerThrAlaValTyrGlyHisPheGlyArgGluGlnPheProTrpGluArg 374

Qy      46 GCCGACTTCACCTGCGAGGTG---------GTCAAGCCC 75
              |||      |||::::::         |||:::|||
Db     375 ThrAspCysValCysAspLeuGlnArgAlaValArgPro 387

RESULT 39
A47151
methionine adenosyltransferase (EC 2.5.1.6) - mouse
N;Alternate names: S-adenosylmethionine synthetase
C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-May-2000
C;Accession: A47151
R;Sakata, S.F.; Shelly, L.L.; Ruppert, S.; Schutz, G.; Chou, J.Y.
J. Biol. Chem. 268, 13978-13986, 1993
A;Title: Cloning and expression of murine S-adenosylmethionine synthetase.
A;Reference number: A47151; MUID:93300783; PMID:8314764
A;Accession: A47151
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-396 <SAK>
A;Experimental source: liver
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:134412, NCBIP:134413)
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:                1.93        Length:          396
Score:                    59.00       Matches:         13
Percent Similarity:       71.43%      Conservative:    2
Best Local Similarity:    61.90%      Mismatches:      4
```

```
Query Match:            42.75%      Indels:        2
DB:                     2           Gaps:          1

US-09-198-779B-1_COPY_160_235 (1-76) x A47151 (1-396)

Qy     10 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTC 69
          |||||||||   ||||||||||||||||||      :::::::|||      ||||||
Db    374 LysThrAlaCysTyrGlyHisPheGlyArg------SerGluPheProTrpGluValPro 391

Qy     70 AAG 72
          |||
Db    392 Lys 392

RESULT 40
S06114
methionine adenosyltransferase (EC 2.5.1.6) - rat
N;Alternate names: S-adenosylmethionine synthetase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 05-May-2000
C;Accession: S06114; S18256; S18257
R;Horikawa, S.; Ishikawa, M.; Ozasa, H.; Tsukada, K.
Eur. J. Biochem. 184, 497-501, 1989
A;Title: Isolation of a cDNA encoding the rat liver S-adenosylmethionine synthetase.
A;Reference number: S06114; MUID:90032633; PMID:2806235
A;Accession: S06114
A;Molecule type: mRNA
A;Residues: 1-397 <HOR>
A;Cross-references: EMBL:X15734; NID:g57183; PIDN:CAA33754.1; PID:g57184
R;Mato, J.M.
submitted to the EMBL Data Library, July 1991
A;Reference number: S18256
A;Accession: S18256
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-397 <MAT>
A;Cross-references: EMBL:X60822
R;Alvarez, L.; Asuncion, M.; Corrales, F.; Pajares, M.A.; Mato, J.M.
FEBS Lett. 290, 142-146, 1991
A;Title: Analysis of the 5' non-coding region of rat liver S-adenosylmethionine syntheta
A;Reference number: S18257; MUID:92008649; PMID:1915866
A;Accession: S18257
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-46 <ALV>
A;Cross-references: EMBL:X60822
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:              1.93        Length:        397
Score:                  59.00       Matches:       13
Percent Similarity:     71.43%      Conservative:  2
Best Local Similarity:  61.90%      Mismatches:    4
Query Match:            42.75%      Indels:        2
DB:                     2           Gaps:          1

US-09-198-779B-1_COPY_160_235 (1-76) x S06114 (1-397)

Qy     10 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTC 69
          |||||||||   ||||||||||||||||||      :::::::|||      ||||||
Db    375 LysThrAlaCysTyrGlyHisPheGlyArg------SerGluPheProTrpGluValPro 392

Qy     70 AAG 72
          |||
Db    393 Lys 393

RESULT 41
H70866
hypothetical protein Rv2473 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: H70866
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70866
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-238 <COL>
A;Cross-references: GB:AL021246; GB:AL123456; NID:g3261507; PIDN:CAA16050.1; PID:e123
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv2473

Alignment Scores:
Pred. No.:              2.29        Length:        238
Score:                  58.50       Matches:       13
Percent Similarity:     60.87%      Conservative:  1
Best Local Similarity:  56.52%      Mismatches:    4
Query Match:            42.39%      Indels:        5
DB:                     2           Gaps:          1

US-09-198-779B-1_COPY_160_235 (1-76) x H70866 (1-238)

Qy      2 GGTTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCG 61
          |||||||||||||||      :::               |||||||||   ||||||
Db     66 GlySerSerArgProAlaProSer--------------ThrThrProArgSerProGly 80

Qy     62 AGGTGGTCA 70
          |||||||||
Db     81 ArgTrpSer 83

RESULT 42
E84977
methionine adenosyltransferase (EC 2.5.1.6) [imported] - Buchnera sp. (strain APS)
N;Alternate names: S-adenosylmethionine synthetase
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: E84977
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: E84977
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-378 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: metK; BU408
C;Superfamily: methionine adenosyltransferase
C;Keywords: S-adenosylmethionine; transferase

Alignment Scores:
Pred. No.:              2.73        Length:        378
Score:                  58.00       Matches:       9
Percent Similarity:     85.71%      Conservative:  3
Best Local Similarity:  64.29%      Mismatches:    2
Query Match:            42.03%      Indels:        0
DB:                     2           Gaps:          0

US-09-198-779B-1_COPY_160_235 (1-76) x E84977 (1-378)

Qy      4 TTCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGAC 45
          ::::::|||||||||   ||||||||||||||||||   :::
Db    352 TyrLeuLysThrAlaValTyrGlyHisPheGlyArgLysGlu 365

RESULT 43
T13845
microtubule-associated protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
```

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C;Accession: T13845
R;Saunders, R.D.; Avides, M.C.; Howard, T.; Gonzalez, C.; Glover, D.M.
J. Cell Biol. 137, 881-890, 1997
A;Title: The Drosophila gene abnormal spindle encodes a microtubule-associated protein t
A;Reference number: Z17792; MUID:97296495; PMID:9151690
A;Accession: T13845
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1861 <SAU>
A;Cross-references: EMBL:U95171; NID:g1930121; PID:g1930122; PIDN:AAB51540.1
C;Genetics:
A;Gene: asp
A;Cross-references: FlyBase:FBgn0000140
C;Function:
A;Description: is required for the normal function of the mitotic spindle

Alignment Scores:

Pred. No.:	2.72	Length:	1861
Score:	58.00	Matches:	10
Percent Similarity:	58.33%	Conservative:	4
Best Local Similarity:	41.67%	Mismatches:	10
Query Match:	42.03%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x T13845 (1-1861)

```
Qy       5 TCATCAAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGG 64
           ::::::   ||||||         |||      ||||||   ||:::   ||||||
Db      83 AlaAlaAlaProProSerLysGlnThrTrpArgValThrAlaProSerArgProAlaAla 102

Qy      65 TGGTCAAGCCCC 76
           |||:::   |||
Db     103 TrpAlaHisPro 106
```

RESULT 44
AE2211
S-adenosylmethionine synthetase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AE2211
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2211
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74943.1; PID:g17132339; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all3244
C;Superfamily: methionine adenosyltransferase

Alignment Scores:

Pred. No.:	3.85	Length:	394
Score:	57.00	Matches:	11
Percent Similarity:	60.00%	Conservative:	1
Best Local Similarity:	55.00%	Mismatches:	8
Query Match:	41.30%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_160_235 (1-76) x AE2211 (1-394)

```
Qy      10 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTGCGAGGTGGTC 69
           |||   ||||||||||||||   ||||||   |||   |||         |||   :::
Db     369 LysLeuAlaAlaTyrGlyHisValGlyArgGlnAspIleAspLeuProTrpGluLysIle 388
```

RESULT 45
T50705
gamma-aminobutyrate aminotransferase (EC 2.6.1.-) rhbA homolog [imported] - Rhodobact
N;Alternate names: pyridoxal-phosphate dependent aminotransferase
C;Species: Rhodobacter sphaeroides
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C;Accession: T50705
R;Choudhary, M.; Kaplan, S.
Nucleic Acids Res. 28, 862-867, 2000
A;Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroide
A;Reference number: Z25222; MUID:20115911; PMID:10648776
A;Accession: T50705
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-447 <CHO>
A;Cross-references: EMBL:AF195122; PIDN:AAF24249.1
A;Experimental source: strain 2.4.1
C;Genetics:
A;Gene: rhbA
C;Keywords: aminotransferase

Alignment Scores:

Pred. No.:	3.85	Length:	447
Score:	57.00	Matches:	11
Percent Similarity:	55.56%	Conservative:	4
Best Local Similarity:	40.74%	Mismatches:	8
Query Match:	41.30%	Indels:	4
DB:	2	Gaps:	1

US-09-198-779B-1_COPY_160_235 (1-76) x T50705 (1-447)

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Qy       8 TCAAGACCGCCG------------CATACGGCCACTTTGGCCGTGACGACGCCGACTTCA 55
           |||   ||||||            |||       :::         ||||||::::::
Db       5 SerLeuProProArgGlyAlaAlaHisGluProAlaMetProCysArgThrProSerAla 24

Qy      56 CCTGCGAGGTGGTCAAGCCCC 76
           ||||||||||||:::   |||
Db      25 ProAlaArgTrpThrCysPro 31
```

Search completed: April 23, 2003, 12:08:01
Job time : 8.33333 secs

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: April 23, 2003, 12:06:52 ; Search time 89.0694 Seconds
(without alignments)
3059.318 Million cell updates/sec

Title: US-09-198-779B-1_COPY_1_121
Perfect score: 121
Sequence: 1 gttttccgtctagcctcggt.....caggacacaacacgtacgtt 121

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	121	100.0	2061	21	AAA48574	cDNA encoding corn
	2	29.2	24.1	2604	21	AAA48576	cDNA encoding whea
	3	28.8	23.8	705	24	ABQ25086	Oligonucleotide fo
c	4	28.8	23.8	705	24	ABQ25087	Oligonucleotide fo
	5	28.8	23.8	1519	20	AAV64373	GABA-gated chlorid
	6	28.6	23.6	405	23	ABV48454	Human prostate exp
	7	28.2	23.3	297	16	AAQ88698	Beta-amyloid precu
	8	28.2	23.3	300	24	AAK99387	DNA of wild type C
	9	28	23.1	1357	21	AAC79021	Human secreted pro
c	10	27.6	22.8	1086	23	ABL04431	Drosophila melanog
	11	27.6	22.8	3205	23	ABL04430	Drosophila melanog
	12	27.6	22.8	3457	23	ABL04426	Drosophila melanog
c	13	27.4	22.6	4659	23	ABL29895	Drosophila melanog
c	14	27.4	22.6	7643	23	ABL29894	Drosophila melanog
	15	27.4	22.6	32042	20	AAZ09252	Human CARD-4 DNA.
	16	27.4	22.6	32042	22	AAF30011	Human CARD-4 gene.
	17	27.4	22.6	32042	24	AAL40765	Genomic DNA of hum
	18	27	22.3	628	24	ABQ25024	Oligonucleotide fo
c	19	27	22.3	628	24	ABQ25025	Oligonucleotide fo
	20	26.8	22.1	374	23	ABV54453	Human prostate exp
	21	26.8	22.1	408	22	AAI86054	Human polynucleoti
c	22	26.8	22.1	486	21	AAZ97380	Human prostate can
c	23	26.8	22.1	1004	21	AAZ97180	Human prostate can
	24	26.8	22.1	2033	22	AAD03458	Zea mays modified
	25	26.8	22.1	2037	21	AAZ99961	Nucleotide sequenc
c	26	26.8	22.1	2650	22	AAH14585	Human cDNA sequenc
c	27	26.8	22.1	2897	22	AAH16327	Human cDNA sequenc
c	28	26.8	22.1	3095	17	AAT31290	Mouse poly-immunog
c	29	26.8	22.1	13255	23	ABL16634	Drosophila melanog
c	30	26.8	22.1	29392	19	AAV15422	Mouse poly Ig rece
	31	26.8	22.1	33513	22	AAK78746	Human immune/haema
	32	26.6	22.0	294	9	AAN81965	Clone Am4 encoding
	33	26.6	22.0	297	16	AAQ88696	Beta-amyloid precu
	34	26.6	22.0	297	16	AAQ88697	Beta-amyloid precu
	35	26.6	22.0	300	14	AAQ42665	Full-length beta-a
	36	26.6	22.0	300	24	AAK99386	DNA of wild type C
	37	26.6	22.0	303	21	AAA39488	Human APP C100 DNA
	38	26.6	22.0	309	16	AAQ88699	Beta-amyloid precu
	39	26.6	22.0	309	16	AAQ88700	Beta-amyloid precu
	40	26.6	22.0	315	22	AAD20982	Human recombinant
	41	26.6	22.0	327	24	AAD23935	Gamma-secretase su
	42	26.6	22.0	336	17	AAT18082	Familial Alzheimer
	43	26.6	22.0	337	14	AAQ59415	Human brain Expres
	44	26.6	22.0	354	19	AAV07188	Flag-amyloid prote
	45	26.6	22.0	354	19	AAV20379	DNA for APP C-term
	46	26.6	22.0	354	21	AAA39490	Human APP signal p
	47	26.6	22.0	354	22	AAD20981	Human recombinant
	48	26.6	22.0	495	21	AAA39492	Human APP intron,
	49	26.6	22.0	581	22	AAL15643	Human breast cance
	50	26.6	22.0	1062	9	AAN80607	Lambda SM2W3 encod

ALIGNMENTS

RESULT 1
AAA48574
ID AAA48574 standard; cDNA; 2061 BP.
XX
AC AAA48574;
XX
DT 19-SEP-2000 (first entry)
XX
DE cDNA encoding corn protein phosphatase 2A regulatory subunit A.
XX
KW Corn; protein phosphatase 2A; protein phosphorylation modulation;
KW transgenic plant; gene therapy; ss.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
FT CDS 56..1820
FT /*tag= a
FT /product= "protein phosphatase 2A regulatory
FT subunit A"
XX
PN WO200036121-A2.
XX
PD 22-JUN-2000.
XX
PF 15-DEC-1999; 99WO-US29823.
XX

corn

```
PR   16-DEC-1998;   98US-0112541.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Famodu OO,  Miao G,  Sakai H,  Lee J,  Rafalski JA,  Klein TM;
XX
DR   WPI; 2000-431599/37.
DR   P-PSDB; AAY99819.
XX
PT   Polynucleotides encoding plant protein phosphatase useful for
PT   modulating reversible protein phosphorylation in plants -
XX
PS   Claim 4; Page 53-54; 73pp; English.
XX
CC   The present sequence encodes corn protein phosphatase 2A regulatory
CC   subunit A. The sequence was identified in clone p0018.chsug10r:fis of a
CC   cDNA library made from corn ear shoot. BLAST analysis showed that the
CC   present sequence encodes protein phosphatase 2A regulatory subunit A.
CC   The sequence may be used for the recombinant production of the protein
CC   in vivo, e.g. via a gene therapy protocol, or in vitro, e.g. in
CC   fermentation culture. The protein may then be used to modulate the
CC   process of reversible protein phosphorylation in plants. It may be used
CC   directly to supplement a plant's own production of the enzyme or to
CC   rectify mutations that result in the expression of inactive protein.
CC   The protein may also be used to test for modulators of protein
CC   phosphorylation which may be used to alter the activity of the enzyme.
XX
SQ   Sequence 2061 BP; 549 A; 432 C; 498 G; 582 T; 0 other;

  Query Match             100.0%;  Score 121;  DB 21;  Length 2061;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-33;
  Matches  121;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTTTTCCGTCTAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1908 GTTTTCCGTCTAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCC 1967

Qy      61 TGATCCATTGTTCGTTGTGTTATTAATGTTGTATAATTGAGCAGGACACAACACGTACGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1968 TGATCCATTGTTCGTTGTGTTATTAATGTTGTATAATTGAGCAGGACACAACACGTACGT 2027

Qy     121 T 121
          |
Db    2028 T 2028


RESULT 2
AAA48576
ID   AAA48576 standard; cDNA; 2604 BP.
XX
AC   AAA48576;
XX
DT   19-SEP-2000  (first entry)
XX
DE   cDNA encoding wheat protein phosphatase 2A regulatory subunit A.
XX
KW   Wheat; protein phosphatase 2A; protein phosphorylation modulation;
KW   transgenic plant; gene therapy; ss.
XX
OS   Triticum aestivum.
XX
FH   Key             Location/Qualifiers
FT   CDS             101..2028
FT                   /*tag=  a
FT                   /product= "protein phosphatase 2A regulatory
FT                   subunit A"
FT                   /note= "contains an intron"
FT   exon            101..1537
FT                   /*tag=  b
FT                   /number= 1
FT   intron          1538..1794
FT                   /*tag=  c
FT                   /number= 1
FT   exon            1795..2028
FT                   /*tag=  d
FT                   /number= 2
XX
PN   WO200036121-A2.
XX
PD   22-JUN-2000.
XX
PF   15-DEC-1999;   99WO-US29823.
XX
PR   16-DEC-1998;   98US-0112541.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Famodu OO,  Miao G,  Sakai H,  Lee J,  Rafalski JA,  Klein TM;
XX
DR   WPI; 2000-431599/37.
DR   P-PSDB; AAY99821.
XX
PT   Polynucleotides encoding plant protein phosphatase useful for
PT   modulating reversible protein phosphorylation in plants -
XX
PS   Claim 4; Page 59; 73pp; English.
XX
CC   The present sequence encodes wheat protein phosphatase 2A regulatory
CC   subunit A. The sequence was identified in clone wr1.pk0030.b10:fis of a
CC   cDNA library made from the root of a seven-day-old wheat seedling.
CC   BLAST analysis showed that the present sequence encodes protein
CC   phosphatase 2A regulatory subunit A. The sequence may be used
CC   for the recombinant production of the protein in vivo, e.g. via a gene
CC   therapy protocol, or in vitro, e.g. in fermentation culture. The protein
CC   may then be used to modulate the process of reversible protein
CC   phosphorylation in plants. It may be used directly to supplement a
CC   plant's own production of the enzyme or to rectify mutations that result
CC   in the expression of inactive protein. The protein may also be used to
CC   test for modulators of protein phosphorylation which may be used to
CC   alter the activity of the enzyme.
XX
SQ   Sequence 2604 BP; 779 A; 515 C; 579 G; 731 T; 0 other;

  Query Match             24.1%;  Score 29.2;  DB 21;  Length 2604;
  Best Local Similarity   75.8%;  Pred. No. 2.9;
  Matches   50;  Conservative    0;  Mismatches   13;  Indels    3;  Gaps    1;

Qy      38 CCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTAATGTTGTATAAT 97
           |||||||||||  |   ||  ||| |||  | |   |  ||||||||||||||||||
Db    2330 CCATGCTGATAATGGATGGGCTCTGTTCCCCTTT---TGTTGTTATTAATGTTGTATAAT 2386

Qy      98 TGAGCA 103
           ||||||
Db    2387 TGAGCA 2392


RESULT 3
ABQ25086
ID   ABQ25086 standard; DNA; 705 BP.
XX
AC   ABQ25086;
XX
DT   12-JUL-2002  (first entry)
XX
DE   Oligonucleotide for detecting cytosine methylation SEQ ID NO 11677.
XX
KW   Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW   drug; side effect; cancer; central nervous system; cardiovascular;
KW   gastrointestinal; respiratory system; single nucleotide polymorphism;
KW   SNP; cell differentiation; ds.
XX
OS   Homo sapiens.
XX
PN   WO200218632-A2.
XX
PD   07-MAR-2002.
```

```
XX
PF   01-SEP-2001; 2001WO-EP10074.
XX
PR   01-SEP-2000; 2000DE-1043826.
PR   05-SEP-2000; 2000DE-1044543.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K,  Guetig D;
XX
DR   WPI; 2002-371829/40.
XX
PT   Determining the degree of cytosine methylation in genomic DNA, useful
PT   for diagnosis and prognosis, comprises selective hybridization of
PT   amplicons from chemically treated DNA  -
XX
PS   Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC   This invention describes a novel method for determining the degree of
CC   methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC   genomic sample of DNA. The sample is treated chemically to convert
CC   cytosine (C) but not methylated C, to uracil, then part of the genomic
CC   DNA that contains the target C is amplified to form a labeled amplicon.
CC   The amplicon is hybridised to two classes, each with at least one
CC   member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC   and the degree of hybridisation to both classes is determined from the
CC   label on the amplicon. From the ratio of labels hybridised to the two
CC   classes of oligomers, the degree of methylation is calculated. The method
CC   is used: (i) for diagnosis and/or prognosis of side effects of
CC   therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC   of the central nervous, cardiovascular, gastrointestinal and respiratory
CC   systems etc., particularly by detecting mutations or single nucleotide
CC   polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC   types and for investigating cell differentiation. The method allows the
CC   methylation status of many C residues to be determined simultaneously.
CC   ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC   method for determining the degree of cytosine methylation described in
CC   the disclosure of the invention.
XX
SQ   Sequence 705 BP; 156 A; 73 C; 216 G; 260 T; 0 other;

  Query Match             23.8%;  Score 28.8;  DB 24;  Length 705;
  Best Local Similarity   58.0%;  Pred. No. 2.5;
  Matches   51;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy      26 GATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTA 85
           |||||| |  |   ||  || ||||| || | |  |||| | | |||||||| |  ||
Db     469 GATCGAGGTGGTGTATATTGGTAAATAGATGTTGATGATTCGTGGTTCGTTGATTATTTT 528

Qy      86 ATGTTGTATAATTGAGCAGGACACAACA 113
             ||  | | |  ||   || |  || |
Db     529 TAGTATTGTTAACGATGTGGGCGAAATA 556


RESULT 4
ABQ25087/c
ID   ABQ25087 standard; DNA; 705 BP.
XX
AC   ABQ25087;
XX
DT   12-JUL-2002  (first entry)
XX
DE   Oligonucleotide for detecting cytosine methylation SEQ ID NO 11678.
XX
KW   Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW   drug; side effect; cancer; central nervous system; cardiovascular;
KW   gastrointestinal; respiratory system; single nucleotide polymorphism;
KW   SNP; cell differentiation; ds.
XX
OS   Homo sapiens.
XX
PN   WO200218632-A2.
XX
PD   07-MAR-2002.
XX
PF   01-SEP-2001; 2001WO-EP10074.
XX
PR   01-SEP-2000; 2000DE-1043826.
PR   05-SEP-2000; 2000DE-1044543.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K,  Guetig D;
XX
DR   WPI; 2002-371829/40.
XX
PT   Determining the degree of cytosine methylation in genomic DNA, useful
PT   for diagnosis and prognosis, comprises selective hybridization of
PT   amplicons from chemically treated DNA  -
XX
PS   Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC   This invention describes a novel method for determining the degree of
CC   methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC   genomic sample of DNA. The sample is treated chemically to convert
CC   cytosine (C) but not methylated C, to uracil, then part of the genomic
CC   DNA that contains the target C is amplified to form a labeled amplicon.
CC   The amplicon is hybridised to two classes, each with at least one
CC   member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC   and the degree of hybridisation to both classes is determined from the
CC   label on the amplicon. From the ratio of labels hybridised to the two
CC   classes of oligomers, the degree of methylation is calculated. The method
CC   is used: (i) for diagnosis and/or prognosis of side effects of
CC   therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC   of the central nervous, cardiovascular, gastrointestinal and respiratory
CC   systems etc., particularly by detecting mutations or single nucleotide
CC   polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC   types and for investigating cell differentiation. The method allows the
CC   methylation status of many C residues to be determined simultaneously.
CC   ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC   method for determining the degree of cytosine methylation described in
CC   the disclosure of the invention.
XX
SQ   Sequence 705 BP; 260 A; 216 C; 73 G; 156 T; 0 other;

  Query Match             23.8%;  Score 28.8;  DB 24;  Length 705;
  Best Local Similarity   58.0%;  Pred. No. 2.5;
  Matches   51;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy      26 GATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTA 85
           |||||| |  |   ||  || ||||| || | |  |||| | | |||||||| |  ||
Db     237 GATCGAGGTGGTGTATATTGGTAAATAGATGTTGATGATTCGTGGTTCGTTGATTATTTT 178

Qy      86 ATGTTGTATAATTGAGCAGGACACAACA 113
             ||  | | |  ||   || |  || |
Db     177 TAGTATTGTTAACGATGTGGGCGAAATA 150


RESULT 5
AAV64373
ID   AAV64373 standard; cDNA; 1519 BP.
XX
AC   AAV64373;
XX
DT   15-FEB-1999  (first entry)
XX
DE   GABA-gated chloride channel TBW-a3 cDNA.
XX
KW   TBW-a3; GABA-gated chloride channel; tobacco budworm; insecticide;
KW   ss.
XX
OS   Heliothis virescens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1446
FT                   /*tag=  a
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```
FT   sig_peptide     1..66
FT                   /*tag= b
FT   sig_peptide     67..1443
FT                   /*tag= c
XX
PN   WO9849185-A1.
XX
PD   05-NOV-1998.
XX
PF   27-APR-1998;    98WO-US08563.
XX
PR   02-JAN-1998;    98US-0002361.
PR   28-APR-1997;    97US-0044976.
XX
PA   (FMCC ) FMC CORP.
XX
PI   Halling BP,  Yuhas DA;
XX
DR   WPI; 1999-009411/01.
DR   P-PSDB; AAW81635-36.
XX
PT   New isolated Lepidoptera GABA-gated chloride channels - comprise 3
PT   isoforms isolated from the tobacco budworm Heliothis virescens, used
PT   for characterising bioactive agents, e.g. insecticides
XX
PS   Claim 1d; Fig 2; 55pp; English.
XX
CC   This cDNA sequence encompasses the open reading frame encoding
CC   GABA-gated chloride channel TBW-a3 (see AAW81635-36) of tobacco
CC   budworm (Heliothis virescens).  TBW-a3, TBW-a2 (see AAW81633-34)
CC   and TBW-a1 (see AAW81637) proteins are 3 receptor isoforms that show
CC   sequence homology to each other and to other insect GABA-gated
CC   chloride channels.  TBW-2a cDNA was obtained from H. virescens 4th
CC   instar larva RNA by PCR and RACE amplifications.  The invention
CC   provides expression vectors in which a nucleic acid encoding a
CC   GABA-gated chloride channel is driven by an inducible promoter, and
CC   a claimed process for producing a GABA-gated chloride channel by
CC   transformed cells.   The GABA-gated channels or cells expressing
CC   them can be used for characterising a bioactive agent (claimed),
CC   e.g. for use as an insecticide.  Probes and primers that identify
CC   or amplify GABA-gated chloride channel nucleic acids of the
CC   invention are also claimed.
XX
SQ   Sequence 1519 BP; 421 A; 362 C; 347 G; 388 T; 1 other;

  Query Match             23.8%;  Score 28.8;  DB 20;  Length 1519;
  Best Local Similarity   52.5%;  Pred. No. 3.3;
  Matches   63;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy       2 TTTTCCGTCTAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCT 61
           |||| | ||   |     ||||| ||||  || |   ||| |  | |||    |||   |
Db     253 TTTTACTTCAGACAATTTTGGACTGATCCTCGATTAGCATACAAAAAAAGAACCGGAGTT 312

Qy      62 GATCCATTGTTCGTTGTGTTATTAATGTTGTATAATTGAGCAGGACACAACACGTACGTT 121
           ||  | || |  || |  | |  | |  |  | ||   |   | || | |||||| | ||
Db     313 GAAACTTTATCTGTGGGCTCAGAATTCATAAAGAACATATGGGTACCCGACACGTTCTTT 372


RESULT 6
ABV48454
ID   ABV48454 standard; cDNA; 405 BP.
XX
AC   ABV48454;
XX
DT   17-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 48445.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US05171.
XX
PR   17-FEB-2000; 2000US-183319P.
PR   16-MAR-2000; 2000US-189862P.
PR   25-MAY-2000; 2000US-207454P.
PR   09-JUN-2000; 2000US-211314P.
PR   18-JUL-2000; 2000US-219007P.
PR   13-DEC-2000; 2000US-255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Endege WO,  Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS   Claim 1; Page 9499; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for:
CC   (a) assessing whether a patient is afflicted with prostate cancer;
CC   (b) monitoring the progression of prostate cancer in a patient;
CC   (c) assessing the efficacy of a test compound to inhibit prostate
CC   cancer in a patient;
CC   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC   in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound;
CC   (g) determining whether prostate cancer has metastasized in a patient;
CC   (h) assessing the aggressiveness or indolence of prostate cancer in a
CC   patient;
CC   (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ   Sequence 405 BP; 106 A; 86 C; 102 G; 111 T; 0 other;

  Query Match             23.6%;  Score 28.6;  DB 23;  Length 405;
  Best Local Similarity   59.0%;  Pred. No. 2.4;
  Matches   49;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy       9 TCTAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCAT 68
             | ||||  | |||  |       ||  ||   |||||||  ||   || || |  ||||||
Db     321 TATAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAGAAAAAACCGTACCCATCCAT 380

Qy      69 TGTTCGTTGTGTTATTAATGTTG 91
           | ||| | ||||  |  | ||||
Db     381 TCTTCATGGTGTGGTGGAAGTTG 403


RESULT 7
AAQ88698
ID   AAQ88698 standard; cDNA to mRNA; 297 BP.
XX
AC   AAQ88698;
XX
DT   11-NOV-1995  (first entry)
XX
DE   Beta-amyloid precursor protein C-terminal peptide mutant gene.
XX
KW   Human; beta-amyloid precursor protein mutant; C-terminal peptide;
KW   gene transfer; transgenic animal; Alzheimer disease model;
KW   gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP653154-A.
```

XX
PD 17-MAY-1995.
XX
PF 07-NOV-1994; 94EP-0117512.
XX
PR 12-NOV-1993; 93JP-0306026.
XX
PA (FARH) HOECHST JAPAN LTD.
PA (FARH) HOECHST JAPAN KK.
XX
PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;
XX
DR WPI; 1995-180492/24.
DR P-PSDB; AAR74696.
XX
PT Transgenic animal model for Alzheimer's disease - contains DNA encoding
PT part of beta-amyloid precursor protein in a gene construct designed for
PT over-expression in various cell types
XX
PS Claim 2; Page 13-14; 32pp; English.
XX
CC The sequence encodes a human brain beta-amyloid precursor protein
CC (APP) mutant C-terminal peptide, and differs from AAQ88696 by
CC conversion of Val to Ile at codon-46. The DNA may be transferred
CC along with an APP signal peptide gene (e.g. AAQ88695) into somatic and
CC germ cells of a non-human mammal, and the resulting transgenic animal
CC may be used as a model for Alzheimer disease (AD). The animal model
CC exhibits symptoms similar to AD, producing large quantities of APP
CC C-terminal peptide, death of neuron cells in pyrimidal cells at
CC cerebral amyloid regions, increases in glial cells and deposition
CC of abnormally phosphorylated tau protein. The animal model may
CC be used to develop new therapies for AD, including gene therapy
CC strategies.
XX
SQ Sequence 297 BP; 87 A; 64 C; 77 G; 69 T; 0 other;

Query Match 23.3%; Score 28.2; DB 16; Length 297;
Best Local Similarity 59.3%; Pred. No. 3.1;
Matches 48; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 11 TAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTG 70
|||| | ||| || || ||||||| || || || | |||||||
Db 122 TAGCGACAGTGATCATCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCATTC 181

Qy 71 TTCGTTGTGTTATTAATGTTG 91
|| | |||| | | ||||
Db 182 ATCATGGTGTGGTGGAGGTTG 202

RESULT 8
AAK99387
ID AAK99387 standard; DNA; 300 BP.
XX
AC AAK99387;
XX
DT 27-JUN-2002 (first entry)
XX
DE DNA of wild type C99 portion of human APP with the London mutation.
XX
KW Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta;
KW amyloid precursor protein; tissue-specific expression control; human APP;
KW APP pathway modulator; gene therapy; mutant; ds.
XX
OS Homo sapiens.
XX
PN WO200226820-A2.
XX
PD 04-APR-2002.
XX
PF 01-OCT-2001; 2001WO-EP11345.
XX
PR 29-SEP-2000; 2000US-236893P.
PR 14-JUN-2001; 2001US-298309P.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;
PI Reinhardt MWHM, Zusman S;
XX
DR WPI; 2002-315796/35.
XX
PT New transgenic fly, containing DNA encoding an Abeta portion of human
PT APP, useful for identifying agents which modulate the APP pathway and
PT which can be used to treat Alzheimer's disease -
XX
PS Claim 4; Page 84; 129pp; English.
XX
CC The invention relates to a transgenic fly whose genome comprises DNA
CC encoding a polypeptide having the Abeta portion of human amyloid
CC precursor protein (APP), fused to a signal sequence. The DNA sequence
CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
CC the specification. The DNA sequence is operably linked to a tissue-
CC specific expression control sequence. Expression of the sequence gives
CC the fly an altered phenotype. The purpose of the invention is for
CC identifying agents that inhibit or promote the expression and/or function
CC of genes or encoded polypeptides which modify the APP pathway. The agent
CC is a compound, triple helix DNA, antisense oligonucleotide, double
CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used
CC to treat conditions such as Alzheimer's disease. The agent can be used as
CC an APP pathway modulator or in gene therapy. This polynucleotide sequence
CC represents the DNA of the wild type C99 portion of human APP with the
CC London mutation of the invention.
XX
SQ Sequence 300 BP; 88 A; 65 C; 78 G; 69 T; 0 other;

Query Match 23.3%; Score 28.2; DB 24; Length 300;
Best Local Similarity 59.3%; Pred. No. 3.1;
Matches 48; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 11 TAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTG 70
|||| | ||| || || ||||||| || || || | |||||||
Db 122 TAGCGACAGTGATCATCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCATTC 181

Qy 71 TTCGTTGTGTTATTAATGTTG 91
|| | |||| | | ||||
Db 182 ATCATGGTGTGGTGGAGGTTG 202

RESULT 9
AAC79021
ID AAC79021 standard; DNA; 1357 BP.
XX
AC AAC79021;
XX
DT 14-FEB-2001 (first entry)
XX
DE Human secreted protein gene 25 clone HODAH24.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein; ss.
XX
OS Homo sapiens.
XX
PN WO200058358-A1.
XX
PD 05-OCT-2000.
XX
PF 23-MAR-2000; 2000WO-US07725.
XX
PR 26-MAR-1999; 99US-0126602.
PR 14-JAN-2000; 2000US-0176063.
XX

```
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM,  Komatsoulis G;
XX
DR   WPI; 2000-594640/56.
DR   P-PSDB; AAB44359.
XX
PT   Fourty nine nucleic acid molecules encoding human secreted proteins,
PT   useful in the prevention, treatment and diagnosis of cancer, immune
PT   disorders, cardiovascular disorders and neurological diseases -
XX
PS   Claim 1; Page 327-328; 367pp; English.
XX
CC   The invention relates to the isolation of genes AAC78997-C79045 encoding
CC   49 human secreted proteins AAB44335-B44382. The genes can be used to
CC   generate fusion proteins by linking to the gene for the human
CC   immunoglobulin G Fc portion (AAC78988) for increasing the stability of
CC   the fusion protein as compared to the human protein only. The genes and
CC   proteins are useful for preventing, ameliorating or treating medical
CC   conditions, e.g. by protein or gene therapy. The genes are isolated
CC   from a range of human tissues disclosed in the specification. The
CC   nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC   the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC   and ovarian cancer, and other cancers of the adrenal gland, bone, bone
CC   marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC   (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC   haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC   disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC   colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d)
CC   wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC   epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC   and parasitic infections.
XX
SQ   Sequence 1357 BP; 386 A; 272 C; 299 G; 398 T; 2 other;

  Query Match             23.1%;  Score 28;  DB 21;  Length 1357;
  Best Local Similarity   52.6%;  Pred. No. 6.1;
  Matches   61;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy       1 GTTTTCCGTCTAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCC 60
           |||  |  | | | || | |  ||  | |   ||  ||||   || | |    || | |
Db     871 GTTACCTTTGTTGACTGGATCCACCCACCTTGGCCTCCCAAAGTGCTGAGATTACAGACG 930

Qy      61 TGATCCATTGTTCGTTGTGTTATTAATGTTGTATAATTGAGCAGGACACAACACGT 116
           ||| |||| || |   |  || | ||| || | |  || |  |     ||||| |
Db     931 TGAGCCATGGTGCCCGGCATTTTAAATTTTTTTTTTTTAATTAATTGCCAACACTT 986


RESULT 10
ABL04431/c
ID   ABL04431 standard; cDNA; 1086 BP.
XX
AC   ABL04431;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 7775.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ss.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   P-PSDB; ABB60328.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Claim 1; SEQ ID NO 7775; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1086 BP; 295 A; 267 C; 273 G; 251 T; 0 other;

  Query Match             22.8%;  Score 27.6;  DB 23;  Length 1086;
  Best Local Similarity   60.8%;  Pred. No. 7.9;
  Matches   45;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy      36 GCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTAATGTTGTATA 95
           ||||||     ||| |||| |||||   ||| | |  |||| |       | ||  || |
Db     943 GCCCATATCCGTAACTGGAGGGTCCCCCTCCGTAGGACGTTATTCCGGCTAGGTAATAAA 884

Qy      96 ATTGAGCAGGACAC 109
           ||||| ||| || |
Db     883 ATTGATCAGCACCC 870


RESULT 11
ABL04430
ID   ABL04430 standard; cDNA; 3205 BP.
XX
AC   ABL04430;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 7772.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ss.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   P-PSDB; ABB60327.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
```

```
XX
PS   Claim 1; SEQ ID NO 7772; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 3205 BP; 932 A; 681 C; 655 G; 937 T; 0 other;

  Query Match             22.8%;  Score 27.6;  DB 23;  Length 3205;
  Best Local Similarity   60.8%;  Pred. No. 12;
  Matches   45;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy      36 GCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTAATGTTGTATA 95
           ||||||     ||| |||| |||||   ||| | |  |||| |       | ||  || |
Db    1199 GCCCATATCCGTAACTGGAGGGTCCCCCTCCGTAGGACGTTATTCCGGCTAGGTAATAAA 1258

Qy      96 ATTGAGCAGGACAC 109
           ||||| ||| || |
Db    1259 ATTGATCAGCACCC 1272


RESULT 12
ABL04426
ID   ABL04426 standard; cDNA; 3457 BP.
XX
AC   ABL04426;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 7760.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ss.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   P-PSDB; ABB60323.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Claim 1; SEQ ID NO 7760; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 3457 BP; 895 A; 779 C; 690 G; 1093 T; 0 other;

  Query Match             22.8%;  Score 27.6;  DB 23;  Length 3457;
  Best Local Similarity   60.8%;  Pred. No. 12;
  Matches   45;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy      36 GCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTAATGTTGTATA 95
           ||||||     ||| |||| |||||   ||| | |  |||| |       | ||  || |
Db    3299 GCCCATATCCGTAACTGGAGGGTCCCCCTCCGTAGGACGTTATTCCGGCTAGGTAATAAA 3358

Qy      96 ATTGAGCAGGACAC 109
           ||||| ||| || |
Db    3359 ATTGATCAGCACCC 3372


RESULT 13
ABL29895/c
ID   ABL29895 standard; DNA; 4659 BP.
XX
AC   ABL29895;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 41158.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Claim 1; SEQ ID NO 41158; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 4659 BP; 1472 A; 1196 C; 1153 G; 838 T; 0 other;

  Query Match             22.6%;  Score 27.4;  DB 23;  Length 4659;
  Best Local Similarity   69.8%;  Pred. No. 16;
```

```
  Matches   37;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy      13 GCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATC 65
           ||| |  | | |||||| |||||| ||| | |||||| |||  ||  ||  ||
Db    4250 GCCACATTTGGCAGATCCACGCTGGCCAAGTTGATAATTGGCTGGGGCTTTTC 4198


RESULT 14
ABL29894/c
ID   ABL29894 standard; DNA; 7643 BP.
XX
AC   ABL29894;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 41155.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Claim 1; SEQ ID NO 41155; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 7643 BP; 2424 A; 1682 C; 1690 G; 1847 T; 0 other;

  Query Match             22.6%;  Score 27.4;  DB 23;  Length 7643;
  Best Local Similarity   69.8%;  Pred. No. 18;
  Matches   37;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy      13 GCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATC 65
           ||| |  | | |||||| |||||| ||| | |||||| |||  ||  ||  ||
Db    6234 GCCACATTTGGCAGATCCACGCTGGCCAAGTTGATAATTGGCTGGGGCTTTTC 6182


RESULT 15
AAZ09252
ID   AAZ09252 standard; DNA; 32042 BP.
XX
AC   AAZ09252;
XX
DT   25-OCT-1999  (first entry)
XX
DE   Human CARD-4 DNA.
XX
KW   CARD-3; caspase recruitment domain; CARD-4; regulation; detection;
KW   caspase activation; detection; screening; therapy; diagnosis; disease;
KW   apoptotic cell death; Fas/APO-1 receptor complex; TNF receptor complex;
KW   cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection;
KW   hormone-dependent tumour; autoimmune disorder; Alzheimer's disease;
KW   systemic lupus erythematosis; immune-mediated glomerulonephritis; stroke;
KW   Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;
KW   spinal muscular dystrophy; cerebellar degeneration; anaemia; drug;
KW   myelodysplastic syndrome; myocardial infarction; cell proliferation;
KW   cell differentiation; cell survival; CARD-4L; CARD-4S; CARD-4Y;
KW   CARD-4Z; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            364..685
FT                   /*tag= a
FT                   /number= 1
FT   CDS             485..31768
FT                   /*tag= b
FT                   /product= "CARD-4"
FT   intron          686..2094
FT                   /*tag= c
FT                   /number= 1
FT   exon            2095..2269
FT                   /*tag= d
FT                   /number= 2
FT   intron          2270..4365
FT                   /*tag= e
FT                   /product= 2
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FT                   /*tag= f
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FT                   /number= 5
FT   intron          10440..11181
FT                   /*tag= k
FT                   /number= 5
FT   exon            11182..11265
FT                   /*tag= l
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FT                   /*tag= m
FT                   /number= 6
FT   exon            19750..19833
FT                   /*tag= n
FT                   /number= 7
FT   intron          19834..21324
FT                   /*tag= o
FT                   /number= 7
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FT                   /*tag= q
FT                   /number= 8
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FT                   /*tag= r
FT                   /number= 9
FT   intron          24311..27948
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FT                   /*tag=  s
FT                   /number= 9
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FT                   /product= 10
FT   intron          28033..31695
FT                   /*tag=  u
FT                   /number= 10
FT   exon            31696..32024
FT                   /*tag=  v
FT                   /number= 11
XX
PN   WO9940102-A1.
XX
PD   12-AUG-1999.
XX
PF   05-FEB-1999;    99WO-US02544.
XX
PR   08-DEC-1998;    98US-0207359.
PR   06-FEB-1998;    98US-0019942.
PR   17-JUN-1998;    98US-0099041.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Bertin J;
XX
DR   WPI; 1999-494269/41.
XX
PT   Novel CARD-3 and CARD-4 genes and polypeptides used or treating
PT   regulation of cellular proliferation and differentiation and cell
PT   survival
XX
PS   Example 13; Fig 18; 181pp; English.
XX
CC   This invention describes the isolation of novel human caspase
CC   recruitment domain, CARD-3 and CARD-4 polynucleotides and proteins and a
CC   partial murine CARD-4L protein and genes. The genes and proteins of
CC   the invention are involved in the regulation of caspase activation.
CC   The caspase recruitment domain (CARD) polynucleotides, polypeptides,
CC   homologues and antibodies can be used in screening assays, detection
CC   assays, predictive medicine and therapeutic and prophylactic methods of
CC   treatment. The methods may be used to diagnose and treat patients which
CC   are suffering from a disorder associated with abnormal level or rate of
CC   apoptotic cell death, abnormal activity of the Fas/APO-1 receptor
CC   complex, abnormal activity of the TNF receptor complex, or abnormal
CC   activity of a caspase. Diseases that may be treated include cancer
CC   (particularly follicular lymphoma, carcinomas associated with mutations
CC   in p53 and hormone-dependent tumours), autoimmune disorders (e.g.
CC   systemic lupus erythematosis, immune-mediated glomerulonephritis), viral
CC   infections, Alzheimer's disease, Parkinson's disease, amyotrophic lateral
CC   sclerosis, retinitis pigmentosa, spinal muscular dystrophy, cerebellar
CC   degeneration, anaemia, myelodysplastic syndrome, myocardial infarction,
CC   and stroke. CARD-3 protein interacts with other cellular proteins, and so
CC   can be used for regulation of cellular proliferation and differentiation
CC   and cell survival. The CARD proteins may also be used to for screen drugs
CC   or compounds which modulate their activity. The CARD-4 gene can express a
CC   long transcript that encodes CARD-4L, a short transcript that encodes
CC   CARD-4S or two CARD-4 splice variants, CARD-4Y and CARD-4Z. This sequence
CC   represents a genomic DNA sequence which encodes the human CARD-4 protein.
XX
SQ   Sequence 32042 BP; 7389 A; 7540 C; 7721 G; 9392 T; 0 other;

  Query Match            22.6%;  Score 27.4;  DB 20;  Length 32042;
  Best Local Similarity  62.3%;  Pred. No. 30;
  Matches   43;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy      28 TCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTAAT 87
           | |||  | ||||| || || | ||   |||||||   ||||||   ||   || || |
Db   18335 TTGACAGTACCCATCCTAATGAGTGTGAGGTCCTGTCTCATTGTGGTTTTGATTCTTGAG 18394

Qy      88 GTTGTATAA 96
           | | | |||
Db   18395 GCTTTTTAA 18403
```

```
RESULT 16
AAF30011
ID   AAF30011 standard; cDNA; 32042 BP.
XX
AC   AAF30011;
XX
DT   23-APR-2001  (first entry)
XX
DE   Human CARD-4 gene.
XX
KW   CARD-4; caspase recruitment domain; human; cancer; infection;
KW   autoimmune disease; neurological disease; haematological disease;
KW   immune disease; inflammation; antitumour; antiseptic;
KW   immunomodulator; antiinflammatory; apoptosis; diagnosis;
KW   gene therapy; chromosome 7; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             485..31768
FT                   /*tag=  a
FT                   /note= "contains introns"
FT   exon            364..685
FT                   /*tag=  b
FT                   /number= 1
FT   intron          686..2094
FT                   /*tag=  c
FT                   /number= 1
FT   exon            2095..2269
FT                   /*tag=  d
FT                   /number= 2
FT   intron          2270..4365
FT                   /*tag=  e
FT                   /number= 2
FT   exon            4366..6190
FT                   /*tag=  f
FT                   /number= 3
FT   intron          6191..9024
FT                   /*tag=  g
FT                   /number= 3
FT   exon            9025..9108
FT                   /*tag=  h
FT                   /number= 4
FT   intron          9109..10355
FT                   /*tag=  i
FT                   /number= 4
FT   exon            10356..10439
FT                   /*tag=  j
FT                   /number= 5
FT   intron          10440..11181
FT                   /*tag=  k
FT                   /number= 5
FT   exon            11182..11265
FT                   /*tag=  l
FT                   /number= 6
FT   intron          11266..19749
FT                   /*tag=  m
FT                   /number= 6
FT   exon            19750..19833
FT                   /*tag=  n
FT                   /number= 7
FT   intron          19834..21324
FT                   /*tag=  o
FT                   /number= 7
FT   exon            21325..21408
FT                   /*tag=  p
FT                   /number= 8
FT   intron          21409..24226
FT                   /*tag=  q
FT                   /number= 8
FT   exon            24227..24310
```

```
FT                   /*tag= r
FT                   /number= 9
FT   intron          24311..27948
FT                   /*tag= s
FT                   /number= 9
FT   exon            27949..28032
FT                   /*tag= t
FT                   /number= 10
FT   intron          28033..31695
FT                   /*tag= u
FT                   /number= 10
FT   exon            31696..32024
FT                   /*tag= v
FT                   /number= 11
XX
PN   WO200100826-A2.
XX
PD   04-JAN-2001.
XX
PF   28-JUN-2000; 2000WO-US17691.
XX
PR   28-JUN-1999;   99US-0340620.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Bertin J;
XX
DR   WPI; 2001-061973/07.
DR   P-PSDB; AAB20080, AAB20081, AAB20082, AAB20083.
XX
PT   Isolated intracellular proteins predicted to be involved in regulating
PT   caspase activation are used for diagnosis and treatment of e.g. cancer,
PT   viral infections, autoimmune diseases, neurological diseases and
PT   haematological disorders -
XX
PS   Example 13; Fig 18; 208pp; English.
XX
CC   The present sequence is that of the human caspase recruitment
CC   domain 4 (CARD-4) gene on chromosome 7.  CARD-4 exists in at least
CC   4 forms, i.e. the long form CARD-4L (see AAB20080), the short form
CC   CARD-4S (see AAB20081), and splice variants CARD-4Y (see AAB20082)
CC   and CARD-4Z (see AAB20082).  It is an intracellular protein
CC   predicted to be involved in regulating caspase activation.  It
CC   activates the NF-kappaB pathway and enhances caspase 9-mediated
CC   cell death.  Methods of diagnosing and treating patients suffering
CC   from a disorder associated with an abnormal level or rate of apoptotic
CC   cell death, abnormal activity of the Fas/APO-1 receptor complex,
CC   abnormal activity of the tumour necrosis factor receptor complex
CC   or abnormal activity of a caspase involve administering a compound
CC   that modulates the expression or activity of CARD-3, CARD-4, CARD-5
CC   or CARD-6 e.g. a small molecule, antisense nucleic acid, ribozyme
CC   or polypeptide.  Such disorders include cancer, viral infection,
CC   autoimmune disorders, neurological diseases, haematological
CC   disorders, inflammatory disorders and immune disorders.  The CARD-4
CC   gene is useful for genetic information and mapping and identifying
CC   mutations, e.g. mutations in splice donor or acceptor sites.
XX
SQ   Sequence 32042 BP; 7389 A; 7540 C; 7721 G; 9392 T; 0 other;

  Query Match             22.6%;  Score 27.4;  DB 22;  Length 32042;
  Best Local Similarity   62.3%;  Pred. No. 30;
  Matches   43;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy      28 TCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTAAT 87
           | |||  | ||||| || || | ||   |||||||   ||||||   ||   || || |
Db   18335 TTGACAGTACCCATCCTAATGAGTGTGAGGTCCTGTCTCATTGTGGTTTTGATTCTTGAG 18394

Qy      88 GTTGTATAA 96
           | | | |||
Db   18395 GCTTTTTAA 18403


RESULT 17
```

```
AAL40765
ID   AAL40765 standard; DNA; 32042 BP.
XX
AC   AAL40765;
XX
DT   27-SEP-2002  (first entry)
XX
DE   Genomic DNA of human CARD-4 SEQ ID No 44.
XX
KW   Cytostatic; virucide; immunomodulatory; neuroprotective; antialzheimers;
KW   cerebroprotective; antiparkinsonian; antisclerotic; ophthalmological;
KW   nootropic; antianaemic; Caspase Recruitment Domain; CARD; CARD-4L; p53;
KW   cancer; CARD-4S; follicular lymphoma; carcinoma; autoimmune disorder;
KW   hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer;
KW   systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease;
KW   anaemia; neutropenia; myelodysplastic syndrome; human; ds.
XX
OS   Homo sapiens.
XX
PN   US6369196-B1.
XX
PD   09-APR-2002.
XX
PF   05-FEB-1999;   99US-0245281.
XX
PR   06-FEB-1998;   98US-0019942.
PR   17-JUN-1998;   98US-0099041.
PR   08-DEC-1998;   98US-0207359.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Bertin J;
XX
DR   WPI; 2002-391988/42.
XX
PT   Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and
PT   CARD-4S) useful for diagnosing and treating e.g. Parkinson's and
PT   Alzheimer's disease, cancers and viral infections -
XX
PS   Disclosure; Fig 18; 116pp; English.
XX
CC   The invention relates to novel isolated Caspase Recruitment Domain (CARD)
CC   polypeptides, CARD-4L and CARD-4S. The CARD proteins of the invention may
CC   be used to treat disorders associated with decreased CARD expression by
CC   supplementing the patient's own production of CARD. Disorders associated
CC   with the expression and activity of CARD include cancers (particularly
CC   follicular lymphomas, carcinomas associated with mutations in p53, and
CC   hormone-dependent tumours such as breast cancer, prostate cancer, and
CC   ovarian cancer), autoimmune disorders (such as systemic lupus
CC   erythematosus, immune-mediated glomerulonephritis), viral infections
CC   (such as those caused by herpes viruses, poxviruses, and adenoviruses),
CC   neurological diseases (such as Alzheimer's disease, Parkinson's
CC   disease, amylotrophic lateral sclerosis (ALS) retinitis pigmentosa,
CC   spinal muscular atrophy, and various forms of cerebellar degeneration),
CC   anaemia associated with chronic disease, aplastic anaemia, chronic
CC   neutropenia, and the myelodysplastic syndromes. This polynucleotide
CC   sequence represents the DNA of a human CARD relating to the invention.
XX
SQ   Sequence 32042 BP; 7389 A; 7540 C; 7721 G; 9392 T; 0 other;

  Query Match             22.6%;  Score 27.4;  DB 24;  Length 32042;
  Best Local Similarity   62.3%;  Pred. No. 30;
  Matches   43;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy      28 TCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTAAT 87
           | |||  | ||||| || || | ||   |||||||   ||||||   ||   || || |
Db   18335 TTGACAGTACCCATCCTAATGAGTGTGAGGTCCTGTCTCATTGTGGTTTTGATTCTTGAG 18394

Qy      88 GTTGTATAA 96
           | | | |||
Db   18395 GCTTTTTAA 18403
```

```
RESULT 18
ABQ25024
ID   ABQ25024 standard; DNA; 628 BP.
XX
AC   ABQ25024;
XX
DT   12-JUL-2002  (first entry)
XX
DE   Oligonucleotide for detecting cytosine methylation SEQ ID NO 11615.
XX
KW   Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW   drug; side effect; cancer; central nervous system; cardiovascular;
KW   gastrointestinal; respiratory system; single nucleotide polymorphism;
KW   SNP; cell differentiation; ds.
XX
OS   Homo sapiens.
XX
PN   WO200218632-A2.
XX
PD   07-MAR-2002.
XX
PF   01-SEP-2001; 2001WO-EP10074.
XX
PR   01-SEP-2000; 2000DE-1043826.
PR   05-SEP-2000; 2000DE-1044543.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K,  Guetig D;
XX
DR   WPI; 2002-371829/40.
XX
PT   Determining the degree of cytosine methylation in genomic DNA, useful
PT   for diagnosis and prognosis, comprises selective hybridization of
PT   amplicons from chemically treated DNA  -
XX
PS   Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC   This invention describes a novel method for determining the degree of
CC   methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC   genomic sample of DNA. The sample is treated chemically to convert
CC   cytosine (C) but not methylated C, to uracil, then part of the genomic
CC   DNA that contains the target C is amplified to form a labeled amplicon.
CC   The amplicon is hybridised to two classes, each with at least one
CC   member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC   and the degree of hybridisation to both classes is determined from the
CC   label on the amplicon. From the ratio of labels hybridised to the two
CC   classes of oligomers, the degree of methylation is calculated. The method
CC   is used: (i) for diagnosis and/or prognosis of side effects of
CC   therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC   of the central nervous, cardiovascular, gastrointestinal and respiratory
CC   systems etc., particularly by detecting mutations or single nucleotide
CC   polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC   types and for investigating cell differentiation. The method allows the
CC   methylation status of many C residues to be determined simultaneously.
CC   ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC   method for determining the degree of cytosine methylation described in
CC   the disclosure of the invention.
XX
SQ   Sequence 628 BP; 161 A; 54 C; 160 G; 253 T; 0 other;

  Query Match             22.3%;  Score 27;  DB 24;  Length 628;
  Best Local Similarity   60.0%;  Pred. No. 11;
  Matches   45;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy      26 GATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTA 85
           |||||| |  |   ||  || ||||| || | |  |||| | | ||||||||  |  ||
Db     509 GATCGAGGTGGTGTATATTGGTAAATAGATGTTGATGATTCGTGGTTCGTTGATTATTTT 568

Qy      86 ATGTTGTATAATTGA 100
              ||  | | |  ||
Db     569 TAGTATTGTTAACGA 583
```

```
RESULT 19
ABQ25025/c
ID   ABQ25025 standard; DNA; 628 BP.
XX
AC   ABQ25025;
XX
DT   12-JUL-2002  (first entry)
XX
DE   Oligonucleotide for detecting cytosine methylation SEQ ID NO 11616.
XX
KW   Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW   drug; side effect; cancer; central nervous system; cardiovascular;
KW   gastrointestinal; respiratory system; single nucleotide polymorphism;
KW   SNP; cell differentiation; ds.
XX
OS   Homo sapiens.
XX
PN   WO200218632-A2.
XX
PD   07-MAR-2002.
XX
PF   01-SEP-2001; 2001WO-EP10074.
XX
PR   01-SEP-2000; 2000DE-1043826.
PR   05-SEP-2000; 2000DE-1044543.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K,  Guetig D;
XX
DR   WPI; 2002-371829/40.
XX
PT   Determining the degree of cytosine methylation in genomic DNA, useful
PT   for diagnosis and prognosis, comprises selective hybridization of
PT   amplicons from chemically treated DNA  -
XX
PS   Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC   This invention describes a novel method for determining the degree of
CC   methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC   genomic sample of DNA. The sample is treated chemically to convert
CC   cytosine (C) but not methylated C, to uracil, then part of the genomic
CC   DNA that contains the target C is amplified to form a labeled amplicon.
CC   The amplicon is hybridised to two classes, each with at least one
CC   member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC   and the degree of hybridisation to both classes is determined from the
CC   label on the amplicon. From the ratio of labels hybridised to the two
CC   classes of oligomers, the degree of methylation is calculated. The method
CC   is used: (i) for diagnosis and/or prognosis of side effects of
CC   therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC   of the central nervous, cardiovascular, gastrointestinal and respiratory
CC   systems etc., particularly by detecting mutations or single nucleotide
CC   polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC   types and for investigating cell differentiation. The method allows the
CC   methylation status of many C residues to be determined simultaneously.
CC   ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC   method for determining the degree of cytosine methylation described in
CC   the disclosure of the invention.
XX
SQ   Sequence 628 BP; 253 A; 160 C; 54 G; 161 T; 0 other;

  Query Match             22.3%;  Score 27;  DB 24;  Length 628;
  Best Local Similarity   60.0%;  Pred. No. 11;
  Matches   45;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy      26 GATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTA 85
           |||||| |  |   ||  || ||||| || | |  |||| | | ||||||||  |  ||
Db     120 GATCGAGGTGGTGTATATTGGTAAATAGATGTTGATGATTCGTGGTTCGTTGATTATTTT 61

Qy      86 ATGTTGTATAATTGA 100
              ||  | | |  ||
Db      60 TAGTATTGTTAACGA 46
```

```
RESULT 20
ABV54453
ID   ABV54453 standard; cDNA; 374 BP.
XX
AC   ABV54453;
XX
DT   17-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 54444.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US05171.
XX
PR   17-FEB-2000; 2000US-183319P.
PR   16-MAR-2000; 2000US-189862P.
PR   25-MAY-2000; 2000US-207454P.
PR   09-JUN-2000; 2000US-211314P.
PR   18-JUL-2000; 2000US-219007P.
PR   13-DEC-2000; 2000US-255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Endege WO,  Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer  -
XX
PS   Claim 1; Page 10526; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for:
CC   (a) assessing whether a patient is afflicted with prostate cancer;
CC   (b) monitoring the progression of prostate cancer in a patient;
CC   (c) assessing the efficacy of a test compound to inhibit prostate
CC   cancer in a patient;
CC   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC   in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound;
CC   (g) determining whether prostate cancer has metastasized in a patient;
CC   (h) assessing the aggressiveness or indolence of prostate cancer in a
CC   patient;
CC   (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ   Sequence 374 BP; 95 A; 109 C; 80 G; 90 T; 0 other;

  Query Match            22.1%;  Score 26.8;  DB 23;  Length 374;
  Best Local Similarity  61.4%;  Pred. No. 11;
  Matches   43;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy      21 GGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGT 80
           | ||||| | ||||  ||  | | |||||  || ||  || |||| | | |  |||
Db     275 GAACAGACCTACGCATCCTCTTCCGATAACAGGTCGTCCCAGATCAAATCTCAGTTCCAC 334

Qy      81 TATTAATGTT 90
           | | |||| |
Db     335 TCTAAATGCT 344
```

```
RESULT 21
AAI86054
ID   AAI86054 standard; cDNA; 408 BP.
XX
AC   AAI86054;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 6114.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorders; arthritis; inflammation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200164835-A2.
XX
PD   07-SEP-2001.
XX
PF   26-FEB-2001; 2001WO-US04927.
XX
PR   28-FEB-2000; 2000US-0515126.
PR   18-MAY-2000; 2000US-0577409.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-514838/56.
DR   P-PSDB; AAO06123.
XX
PT   Isolated nucleic acids and polypeptides, useful for preventing
PT   diagnosing and treating e.g. leukaemia, inflammation and immune
PT   disorders -
XX
PS   Claim 1; SEQ ID NO 6114; 1399pp + Sequence Listing; English.
XX
CC   The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC   the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 408 BP; 142 A; 55 C; 89 G; 121 T; 1 other;

  Query Match            22.1%;  Score 26.8;  DB 22;  Length 408;
  Best Local Similarity  59.0%;  Pred. No. 11;
  Matches   46;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy      44 TGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTAATGTTGTATAATTGAGCA 103
           | | ||  ||| ||    ||   | ||   ||||| || ||  | || ||| ||  ||||
Db     209 TAAAAAGAGGAGGGGAGAGAGAAAATGGATGTTGTATTCTTGGTTTTATATTATATAGCA 268

Qy     104 GGACACAACACGTACGTT 121
           ||||     | ||| |||
Db     269 GGACTTTTTAAGTAAGTT 286
```

```
RESULT 22
AAZ97380/c
ID   AAZ97380 standard; cDNA; 486 BP.
XX
```

```
AC   AAZ97380;
XX
DT   18-APR-2000  (first entry)
XX
DE   Human prostate cancer differentially expressed gene #241.
XX
KW   Prostate cancer specific gene; cancer; tumour progression; diagnose;
KW   hyperproliferative cell growth; prostatic disorder; treatment;
KW   metastatic prostate cancer; benign prostate hyperplasia; BPH; ss.
XX
OS   Homo sapiens.
XX
PN   WO9964594-A2.
XX
PD   16-DEC-1999.
XX
PF   10-JUN-1999;   99WO-US13181.
XX
PR   11-JUN-1998;   98US-0088877.
PR   09-JUN-1999;   99US-0088877.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Astel JH,  Carroll E,  Endege WO,  Ford DM,  Monahan JE,  Schlegel R;
PI   Steinmann KE,  Zhang J;
XX
DR   WPI; 2000-116541/10.
XX
PT   New isolated prostate cancer specific nucleic acids, used to develop
PT   products for the diagnosis and treatment of cancer -
XX
PS   Claim 2; Page 173; 212pp; English.
XX
CC   This sequence represents a prostate cancer specific nucleic acid
CC   sequence. The invention relates to a method for diagnosing cancer,
CC   tumour progression, hyperproliferative cell growth or accompanying
CC   biological and physical manifestations. The method involves contacting
CC   the biological sample with a probe that comprises a sequence capable of
CC   hybridising to any of the 339 nucleotide sequences given in the
CC   specification (see AAZ97140-Z97478) and detecting duplex formation. The
CC   products and methods of the invention can be used for the diagnosis,
CC   prognosis, and treatment of cancer, tumour progression,
CC   hyperproliferative cell growth, and accompanying physical and biological
CC   manifestations. They can be used particularly for prostatic disorders
CC   such as metastatic prostate cancer, localised prostate cancer, or benign
CC   prostate hyperplasia (BPH).
XX
SQ   Sequence 486 BP; 137 A; 111 C; 128 G; 108 T; 2 other;

  Query Match             22.1%;  Score 26.8;  DB 21;  Length 486;
  Best Local Similarity   59.0%;  Pred. No. 12;
  Matches   46;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy      33 GCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTAATGTTGT 92
           ||| || |  ||| |  |   || ||| ||| ||| ||| | | || | || ||  || |
Db     303 GCTTCCTAAACTGCTGGAATTACAGTCGTGAGCCACTGTGCCTGGTCTCATAAAACTTTT 244

Qy      93 ATAATTGAGCAGGACACA 110
           | | |  | ||    |||
Db     243 AAATTCCATCACATTACA 226


RESULT 23
AAZ97180/c
ID   AAZ97180 standard; cDNA; 1004 BP.
XX
AC   AAZ97180;
XX
DT   18-APR-2000  (first entry)
XX
DE   Human prostate cancer differentially expressed gene #41.
XX
KW   Prostate cancer specific gene; cancer; tumour progression; diagnose;
KW   hyperproliferative cell growth; prostatic disorder; treatment;
KW   metastatic prostate cancer; benign prostate hyperplasia; BPH; ss.
XX
OS   Homo sapiens.
XX
PN   WO9964594-A2.
XX
PD   16-DEC-1999.
XX
PF   10-JUN-1999;   99WO-US13181.
XX
PR   11-JUN-1998;   98US-0088877.
PR   09-JUN-1999;   99US-0088877.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Astel JH,  Carroll E,  Endege WO,  Ford DM,  Monahan JE,  Schlegel R;
PI   Steinmann KE,  Zhang J;
XX
DR   WPI; 2000-116541/10.
XX
PT   New isolated prostate cancer specific nucleic acids, used to develop
PT   products for the diagnosis and treatment of cancer -
XX
PS   Claim 2; Page 89; 212pp; English.
XX
CC   This sequence represents a prostate cancer specific nucleic acid
CC   sequence. The invention relates to a method for diagnosing cancer,
CC   tumour progression, hyperproliferative cell growth or accompanying
CC   biological and physical manifestations. The method involves contacting
CC   the biological sample with a probe that comprises a sequence capable of
CC   hybridising to any of the 339 nucleotide sequences given in the
CC   specification (see AAZ97140-Z97478) and detecting duplex formation. The
CC   products and methods of the invention can be used for the diagnosis,
CC   prognosis, and treatment of cancer, tumour progression,
CC   hyperproliferative cell growth, and accompanying physical and biological
CC   manifestations. They can be used particularly for prostatic disorders
CC   such as metastatic prostate cancer, localised prostate cancer, or benign
CC   prostate hyperplasia (BPH).
XX
SQ   Sequence 1004 BP; 266 A; 208 C; 218 G; 259 T; 53 other;

  Query Match             22.1%;  Score 26.8;  DB 21;  Length 1004;
  Best Local Similarity   59.0%;  Pred. No. 15;
  Matches   46;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy      33 GCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTAATGTTGT 92
           ||| || |  ||| |  |   || ||| ||| ||| ||| | | || | || ||  || |
Db     299 GCTTCCTAAACTGCTGGAATTACAGTCGTGAGCCACTGTGCCTGGTCTCATAAAACTTTT 240

Qy      93 ATAATTGAGCAGGACACA 110
           | | |  | ||    |||
Db     239 AAATTCCATCACATTACA 222


RESULT 24
AAD03458
ID   AAD03458 standard; DNA; 2033 BP.
XX
AC   AAD03458;
XX
DT   13-JUN-2001  (first entry)
XX
DE   Zea mays modified ubiquitin regulatory system (mURS) DNA.
XX
KW   Maize; modified ubiquitin regulatory system; mURS; heatshock element;
KW   transgenic plant; gene regulation; ds.
XX
OS   Zea mays.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    718..723
FT                   /*tag= a
```

```
FT                   /label= "KpnI_site"
FT                   /note= "Replaces the overlapping heatshock elements
FT                   in the wild-type URS"
XX
PN   WO200118220-A1.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-EP08690.
XX
PR   09-SEP-1999;   99EP-0307158.
XX
PA   (MONS ) MONSANTO PLC.
XX
PI   Goldsbrough A;
XX
DR   WPI; 2001-235203/24.
XX
PT   DNA sequence comprising a ubiquitin regulatory system, which lacks
PT   heatshock elements or is not heat inducible, useful for transforming
PT   plants (e.g. corn, wheat or barley) and regulating the expression of a
PT   structural gene under its control -
XX
PS   Claim 4; Fig 3; 39pp; English.
XX
CC   The present sequence is Zea mays modified ubiquitin regulatory system
CC   (mURS) DNA which lacks heatshock elements or is not heat inducible.
CC   The mURS DNA sequence is useful for transforming cells, particularly
CC   plant cells and creating transgenic plants. It is useful for regulating
CC   the expression of a structural gene, particularly when stressed with
CC   elevated temperature. The expression of associated DNA sequences, which
CC   is mediated by the present ubiquitin regulatory system, in transformed
CC   plant cells is stable and not influenced by environmental changes in
CC   temperature, which would normally affect expression mediated by a
CC   non-modified system.
XX
SQ   Sequence 2033 BP; 488 A; 424 C; 423 G; 698 T; 0 other;

  Query Match             22.1%;  Score 26.8;  DB 22;  Length 2033;
  Best Local Similarity   53.9%;  Pred. No. 19;
  Matches   55;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy      3 TTTCCGTCTAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTG 62
          | ||  |||||  | |||  |||  | || || |    | |||||  ||  || |   ||
Db   1493 TATCGATCTAGGATAGGTATACATGTTGATGCGGGTTTTACTGATGCATATACAGAGATG 1552

Qy     63 ATCCATTGTTCGTTGTGTTATTAATGTTGTATAATTGAGCAG 104
            |    |   | | ||  |  | |||| || |  ||| || |
Db   1553 CTTTTGTTCGCTTGGTTGTGATGATGTGGTGTGGTTGGGCGG 1594


RESULT 25
AAZ99961
ID   AAZ99961 standard; DNA; 2037 BP.
XX
AC   AAZ99961;
XX
DT   25-JUL-2000  (first entry)
XX
DE   Nucleotide sequence of a cloned fragment of p97-U3.
XX
KW   Wheat; starch branching enzyme II; SBEII; SBEII-1; starch; SBEII-2;
KW   gelatinisation onset; transgenic plant; foodstuff; bakery product; ds.
XX
OS   Zea mays.
XX
PN   WO200015810-A1.
XX
PD   23-MAR-2000.
XX
PF   09-SEP-1999;   99WO-GB03011.
XX
PR   10-SEP-1998;   98EP-0307337.
XX
PA   (PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.
XX
PI   Goldsbrough A,  Colliver S;
XX
DR   WPI; 2000-271446/23.
XX
PT   DNA encoding wheat starch branching enzyme II isoforms, useful in
PT   altering the characteristics of a plant, especially elevated starch
PT   gelatinization onset and/or peak temperature -
XX
PS   Disclosure; Fig 29; 197pp; English.
XX
CC   The present sequence represents a cloned fragment of p97-U3, which
CC   is used in the course of the invention. The specification describes novel
CC   subclasses of wheat starch branching enzyme II (SBEII), designated
CC   SBEII-1 and SBEII-2. The SBEII-1 genes are thought to have similar
CC   functional properties to the maize SBEIIb gene. Starch branching enzymes
CC   catalyse the formation of the alpha-1,6 linkages, creating branch points
CC   in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage
CC   followed by reattachment of the released alpha-1,4-glucan chain to the
CC   same or another glucosyl chain. SBEII polypeptides can be used to alter
CC   the characteristics of a plant, in particular to alter starch so that
CC   it has an elevated gelatinisation onset and/or peak temperature. Starch
CC   obtained from transgenic plants is useful in the preparation or
CC   processing a foodstuff, particularly bakery products.
XX
SQ   Sequence 2037 BP; 488 A; 426 C; 423 G; 700 T; 0 other;

  Query Match             22.1%;  Score 26.8;  DB 21;  Length 2037;
  Best Local Similarity   53.9%;  Pred. No. 19;
  Matches   55;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy      3 TTTCCGTCTAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTG 62
          | ||  |||||  | |||  |||  | || || |    | |||||  ||  || |   ||
Db   1495 TATCGATCTAGGATAGGTATACATGTTGATGCGGGTTTTACTGATGCATATACAGAGATG 1554

Qy     63 ATCCATTGTTCGTTGTGTTATTAATGTTGTATAATTGAGCAG 104
            |    |   | | ||  |  | |||| || |  ||| || |
Db   1555 CTTTTGTTCGCTTGGTTGTGATGATGTGGTGTGGTTGGGCGG 1596


RESULT 26
AAH14585/c
ID   AAH14585 standard; cDNA; 2650 BP.
XX
AC   AAH14585;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA sequence SEQ ID NO:12185.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
```

```
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 8; SEQ ID 12185; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 2650 BP; 849 A; 495 C; 607 G; 699 T; 0 other;

  Query Match             22.1%;  Score 26.8;  DB 22;  Length 2650;
  Best Local Similarity   59.0%;  Pred. No. 21;
  Matches   46;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy      33 GCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTAATGTTGT 92
           ||| || |  ||| |  |   || ||| ||| ||| ||| | | || | || ||  || |
Db    1858 GCTTCCTAAACTGCTGGAATTACAGTCGTGAGCCACTGTGCCTGGTCTCATAAAACTTTT 1799

Qy      93 ATAATTGAGCAGGACACA 110
           | | |  | ||    |||
Db    1798 AAATTCCATCACATTACA 1781


RESULT 27
AAH16327/c
ID   AAH16327 standard; cDNA; 2897 BP.
XX
AC   AAH16327;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA sequence SEQ ID NO:15232.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 8; SEQ ID 15232; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 2897 BP; 882 A; 564 C; 696 G; 755 T; 0 other;

  Query Match             22.1%;  Score 26.8;  DB 22;  Length 2897;
  Best Local Similarity   59.0%;  Pred. No. 22;
  Matches   46;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy      33 GCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTAATGTTGT 92
           ||| || |  ||| |  |   || ||| ||| ||| ||| | | || | || ||  || |
Db    2080 GCTTCCTAAACTGCTGGAATTACAGTCGTGAGCCACTGTGCCTGGTCTCATAAAACTTTT 2021

Qy      93 ATAATTGAGCAGGACACA 110
           | | |  | ||    |||
Db    2020 AAATTCCATCACATTACA 2003


RESULT 28
AAT31290/c
ID   AAT31290 standard; cDNA; 3095 BP.
XX
AC   AAT31290;
XX
DT   24-FEB-1997  (first entry)
XX
DE   Mouse poly-immunoglobulin receptor, cDNA.
XX
KW   Mouse; immunoglobulin; receptor; protection protein; mutans;
KW   heavy chain; antigen binding domain; protection; pathogen;
KW   mucosal; environment; gastrointestinal; passive; immunisation;
KW   Guy's 13 antibody; prevention; dental caries; Streptococcus;
KW   poly; sorbinus; murine; ss.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             85..2400
FT                   /*tag=  a
```

XX
PN WO9621012-A1.
XX
PD 11-JUL-1996.
XX
PF 27-DEC-1995; 95WO-US16889.
XX
PR 04-MAY-1995; 95US-0434000.
PR 30-DEC-1994; 94US-0367395.
XX
PA (PLAN-) PLANT BIOTECHNOLOGY INC.
PA (UNME-) UNITED MEDICAL & DENTAL SCHOOLS GUYS.
PA (PLAN-) PLANET BIOTECHNOLOGY INC.
XX
PI Hiatt AC, Lehner T, Ma JKC;
XX
DR WPI; 1996-333987/33.
DR P-PSDB; AAW03180.
XX
PT Immunoglobulin and protection protein complex and its prodn. in
PT plants - useful for passive immunisation against mucosal antigens,
PT esp. against S. mutans and S. sorbinus to prevent dental caries
XX
PS Disclosure; Pages 117-121; 152pp; English.
XX
CC The present sequence encodes the mouse poly-immunoglobulin (Ig)
CC receptor, a portion of which corresp. to residues 1-627, pref.
CC 1-606, or esp. residues 13-45, 1-120, 110-230, 210-340, 320-450,
CC 440-550, 550-606 or 550-627 comprises a protection protein (PP).
CC The Ig of the invention comprises a PP as above in association with
CC an Ig derived heavy chain, having at least a portion of an antigen
CC (Ag) binding domain. The PP protects the Ig in harsh mucosal, e.g.
CC gastrointestinal, environments, therefore enhancing its
CC effectiveness in passively immunising animals against mucosal
CC pathogens. The Ag binding domain is specifically derived from the
CC Guy's 13 antibody, and the Ig can be used to prevent dental caries
CC by binding, e.g. Streptococcus mutans serotypes c, e and f, or
CC S. sorbinus serotypes d and g.
XX
SQ Sequence 3095 BP; 861 A; 796 C; 784 G; 654 T; 0 other;

Query Match 22.1%; Score 26.8; DB 17; Length 3095;
Best Local Similarity 64.5%; Pred. No. 22;
Matches 40; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

```
Qy      30 GACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTAATGT 89
           |||  |  |||   ||  | ||| || | || |   |||||| ||||  || | ||||||
Db     760 GACCTTCTCCAGCTTGGCAGATGTACAGCCCAGCATCATTGTGCGTTAGGTGACTAATGT 701

Qy      90 TG 91
           ||
Db     700 TG 699
```

RESULT 29
ABL16634/c
ID ABL16634 standard; DNA; 13255 BP.
XX
AC ABL16634;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 1375.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 1375; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13255 BP; 3879 A; 2652 C; 2622 G; 4102 T; 0 other;

Query Match 22.1%; Score 26.8; DB 23; Length 13255;
Best Local Similarity 61.4%; Pred. No. 37;
Matches 43; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

```
Qy      44 TGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTAATGTTGTATAATTGAGCA 103
           |||||   |   | |  |  |  ||| |||| ||||||   | || | |  || || |||
Db    2315 TGATACTCGATTGATAATCGTTAATTTTTCGCTGTGTTCCAATTGCTATGGAAATGGGCA 2256

Qy     104 GGACACAACA 113
           ||||| || |
Db    2255 GGACATAAAA 2246
```

RESULT 30
AAV15422/c
ID AAV15422 standard; DNA; 29392 BP.
XX
AC AAV15422;
XX
DT 11-JUN-1998 (first entry)
XX
DE Mouse poly Ig receptor protein gene.
XX
KW Mouse; poly Ig receptor protein; pIgR protein; pIg; deficiency;
KW knockout mouse; disease model; ds.
XX
OS Mus sp.
XX
PN JP10057066-A.
XX
PD 03-MAR-1998.
XX
PF 19-AUG-1996; 96JP-0217154.
XX
PR 19-AUG-1996; 96JP-0217154.
XX
PA (HONS) YAKULT HONSHA KK.
XX
DR WPI; 1998-254323/23.
XX
PT Mouse pIg receptor protein gene - used for preparing gene knockout
PT mice, useful for study of human poly Ig receptor protein deficiency

```
XX
PS   Claim 1; Page 4-14; 18pp; Japanese.
XX
CC   The present sequence represents the mouse poly Ig receptor protein
CC   gene, which has a 29392 bp sequence. The new gene can be used to
CC   produce a gene knockout mouse, useful as a disease model of human
CC   poly Ig receptor protein deficiency.
XX
SQ   Sequence 29392 BP; 8318 A; 6747 C; 6514 G; 7813 T; 0 other;

  Query Match             22.1%;  Score 26.8;  DB 19;  Length 29392;
  Best Local Similarity   64.5%;  Pred. No. 48;
  Matches   40;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy      30 GACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTAATGT 89
           |||  |  |||   ||  | ||| || | || |   |||||| ||||  || | ||||||
Db   21417 GACCTTCTCCAGCTTGGCAGATGTACAGCCCAGCATCATTGTGCGTTAGGTGACTAATGT 21358

Qy      90 TG 91
           ||
Db   21357 TG 21356


RESULT 31
AAK78746
ID   AAK78746 standard; DNA; 33513 BP.
XX
AC   AAK78746;
XX
DT   07-NOV-2001  (first entry)
XX
DE   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33558.
XX
KW   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW   cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS   Homo sapiens.
XX
PN   WO200157182-A2.
XX
PD   09-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01354.
XX
PR   31-JAN-2000; 2000US-0179065.
PR   04-FEB-2000; 2000US-0180628.
PR   24-FEB-2000; 2000US-0184664.
PR   02-MAR-2000; 2000US-0186350.
PR   16-MAR-2000; 2000US-0189874.
PR   17-MAR-2000; 2000US-0190076.
PR   18-APR-2000; 2000US-0198123.
PR   19-MAY-2000; 2000US-0205515.
PR   07-JUN-2000; 2000US-0209467.
PR   28-JUN-2000; 2000US-0214886.
PR   30-JUN-2000; 2000US-0215135.
PR   07-JUL-2000; 2000US-0216647.
PR   07-JUL-2000; 2000US-0216880.
PR   11-JUL-2000; 2000US-0217487.
PR   11-JUL-2000; 2000US-0217496.
PR   14-JUL-2000; 2000US-0218290.
PR   26-JUL-2000; 2000US-0220963.
PR   26-JUL-2000; 2000US-0220964.
PR   14-AUG-2000; 2000US-0224518.
PR   14-AUG-2000; 2000US-0224519.
PR   14-AUG-2000; 2000US-0225213.
PR   14-AUG-2000; 2000US-0225214.
PR   14-AUG-2000; 2000US-0225266.
PR   14-AUG-2000; 2000US-0225267.
PR   14-AUG-2000; 2000US-0225268.
PR   14-AUG-2000; 2000US-0225270.
PR   14-AUG-2000; 2000US-0225447.
PR   14-AUG-2000; 2000US-0225757.
PR   14-AUG-2000; 2000US-0225758.
PR   14-AUG-2000; 2000US-0225759.
PR   18-AUG-2000; 2000US-0226279.
PR   22-AUG-2000; 2000US-0226681.
PR   22-AUG-2000; 2000US-0226868.
PR   22-AUG-2000; 2000US-0227182.
PR   23-AUG-2000; 2000US-0227009.
PR   30-AUG-2000; 2000US-0228924.
PR   01-SEP-2000; 2000US-0229287.
PR   01-SEP-2000; 2000US-0229343.
PR   01-SEP-2000; 2000US-0229344.
PR   01-SEP-2000; 2000US-0229345.
PR   05-SEP-2000; 2000US-0229509.
PR   05-SEP-2000; 2000US-0229513.
PR   06-SEP-2000; 2000US-0230437.
PR   06-SEP-2000; 2000US-0230438.
PR   08-SEP-2000; 2000US-0231242.
PR   08-SEP-2000; 2000US-0231243.
PR   08-SEP-2000; 2000US-0231244.
PR   08-SEP-2000; 2000US-0231413.
PR   08-SEP-2000; 2000US-0231414.
PR   08-SEP-2000; 2000US-0232080.
PR   08-SEP-2000; 2000US-0232081.
PR   12-SEP-2000; 2000US-0231968.
PR   14-SEP-2000; 2000US-0232397.
PR   14-SEP-2000; 2000US-0232398.
PR   14-SEP-2000; 2000US-0232399.
PR   14-SEP-2000; 2000US-0232400.
PR   14-SEP-2000; 2000US-0232401.
PR   14-SEP-2000; 2000US-0233063.
PR   14-SEP-2000; 2000US-0233064.
PR   14-SEP-2000; 2000US-0233065.
PR   21-SEP-2000; 2000US-0234223.
PR   21-SEP-2000; 2000US-0234274.
PR   25-SEP-2000; 2000US-0234997.
PR   25-SEP-2000; 2000US-0234998.
PR   26-SEP-2000; 2000US-0235484.
PR   27-SEP-2000; 2000US-0235834.
PR   27-SEP-2000; 2000US-0235836.
PR   29-SEP-2000; 2000US-0236327.
PR   29-SEP-2000; 2000US-0236367.
PR   29-SEP-2000; 2000US-0236368.
PR   29-SEP-2000; 2000US-0236369.
PR   29-SEP-2000; 2000US-0236370.
PR   02-OCT-2000; 2000US-0236802.
PR   02-OCT-2000; 2000US-0237037.
PR   02-OCT-2000; 2000US-0237038.
PR   02-OCT-2000; 2000US-0237039.
PR   02-OCT-2000; 2000US-0237040.
PR   13-OCT-2000; 2000US-0239935.
PR   13-OCT-2000; 2000US-0239937.
PR   20-OCT-2000; 2000US-0240960.
PR   20-OCT-2000; 2000US-0241221.
PR   20-OCT-2000; 2000US-0241785.
PR   20-OCT-2000; 2000US-0241786.
PR   20-OCT-2000; 2000US-0241787.
PR   20-OCT-2000; 2000US-0241808.
PR   20-OCT-2000; 2000US-0241809.
PR   20-OCT-2000; 2000US-0241826.
PR   01-NOV-2000; 2000US-0244617.
PR   08-NOV-2000; 2000US-0246474.
PR   08-NOV-2000; 2000US-0246475.
PR   08-NOV-2000; 2000US-0246476.
PR   08-NOV-2000; 2000US-0246477.
PR   08-NOV-2000; 2000US-0246478.
PR   08-NOV-2000; 2000US-0246523.
PR   08-NOV-2000; 2000US-0246524.
PR   08-NOV-2000; 2000US-0246525.
PR   08-NOV-2000; 2000US-0246526.
PR   08-NOV-2000; 2000US-0246527.
PR   08-NOV-2000; 2000US-0246528.
PR   08-NOV-2000; 2000US-0246532.
PR   08-NOV-2000; 2000US-0246609.
PR   08-NOV-2000; 2000US-0246610.
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PR   08-NOV-2000; 2000US-0246611.
PR   08-NOV-2000; 2000US-0246613.
PR   17-NOV-2000; 2000US-0249207.
PR   17-NOV-2000; 2000US-0249208.
PR   17-NOV-2000; 2000US-0249209.
PR   17-NOV-2000; 2000US-0249210.
PR   17-NOV-2000; 2000US-0249211.
PR   17-NOV-2000; 2000US-0249212.
PR   17-NOV-2000; 2000US-0249213.
PR   17-NOV-2000; 2000US-0249214.
PR   17-NOV-2000; 2000US-0249215.
PR   17-NOV-2000; 2000US-0249216.
PR   17-NOV-2000; 2000US-0249217.
PR   17-NOV-2000; 2000US-0249218.
PR   17-NOV-2000; 2000US-0249244.
PR   17-NOV-2000; 2000US-0249245.
PR   17-NOV-2000; 2000US-0249264.
PR   17-NOV-2000; 2000US-0249265.
PR   17-NOV-2000; 2000US-0249297.
PR   17-NOV-2000; 2000US-0249299.
PR   17-NOV-2000; 2000US-0249300.
PR   01-DEC-2000; 2000US-0250160.
PR   01-DEC-2000; 2000US-0250391.
PR   05-DEC-2000; 2000US-0251030.
PR   05-DEC-2000; 2000US-0251988.
PR   05-DEC-2000; 2000US-0256719.
PR   06-DEC-2000; 2000US-0251479.
PR   08-DEC-2000; 2000US-0251856.
PR   08-DEC-2000; 2000US-0251868.
PR   08-DEC-2000; 2000US-0251869.
PR   08-DEC-2000; 2000US-0251989.
PR   08-DEC-2000; 2000US-0251990.
PR   11-DEC-2000; 2000US-0254097.
PR   05-JAN-2001; 2001US-0259678.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-483426/52.
XX
PT   Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT   useful for preventing, diagnosing and/or treating cancers and
PT   metastasis -
XX
PS   Disclosure; SEQ ID NO 33558; 3071pp + Sequence Listing; English.
XX
CC   AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC   amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC   activity, and can be used in gene therapy and vaccine production. (I)
CC   proteins and polynucleotides may be used in the prevention, diagnosis and
CC   treatment of diseases associated with inappropriate (I) expression. For
CC   example, they may be used to treat disorders associated with decreased
CC   expression by rectifying mutations or deletions in a patient's genome
CC   that affect the activity of (I) by expressing inactive proteins or to
CC   supplement the patients own production of (I). Additionally, (I)
CC   polynucleotides may be used to produce the secreted (I), by inserting
CC   the nucleic acids into a host cell and culturing the cell to express the
CC   protein. (I) proteins and polynucleotides may be used to prevent,
CC   diagnose and treat immune/haematopoietic-related diseases, especially
CC   cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC   to AAK87694 represent human immune/haematopoietic antigen genomic
CC   sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC   represent sequences used in the exemplification of the present invention.
XX
SQ   Sequence 33513 BP; 10336 A; 6612 C; 6676 G; 9889 T; 0 other;

  Query Match             22.1%;  Score 26.8;  DB 22;  Length 33513;
  Best Local Similarity   59.0%;  Pred. No. 51;
  Matches   46;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy    33 GCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTATTAATGTTGT 92
        ||| || |  ||| |  |   || ||| ||| ||| ||| | | || | || || || |
Db 11667 GCTTCCTAAACTGCTGGAATTACAGTCGTGAGCCACTGTGCCTGGTCTCATAAAACTTTT 11726

Qy    93 ATAATTGAGCAGGACACA 110
         | | |  | ||    |||
Db 11727 AAATTCCATCACATTACA 11744


RESULT 32
AAN81965
ID   AAN81965 standard; DNA; 294 BP.
XX
AC   AAN81965;
XX
DT   17-DEC-2001  (updated)
DT   08-OCT-1990  (first entry)
XX
DE   Clone Am4 encoding brain amyloid of Alzheimer's disease and adult
DE   Down's syndrome.
XX
KW   Clone Am4; beta amyloid; Alzheimer's disease; adult Down's syndrome; ss.
XX
PN   USN7019001-N.
XX
PD   27-OCT-1987.
XX
PF   26-FEB-1987;   87US-0091001.
XX
PR   26-FEB-1987;   87US-0091001.
XX
PA   (USSH ) US DEPT HEALTH AND HUMAN.
XX
DR   WPI; 1988-021389/03.
DR   P-PSDB; P981517.
XX
PT   cDNA clone encoding amyloid polypeptide of Alzheimer's disease -
PT   obtd. from adult human brain cDNA library using oligonucleotide
PT   probe.
XX
PS   Disclosure; ; p; English.
XX
CC   The clone encodes the beta amyloid protein found in Alzheimer's disease.
CC   It can be used to study neuropathological changes in Alzheimer's, adult
CC   Down's syndrome, Guamanian amyotrophic lateral sclerosis/Parkinsonism-
CC   dementia and the ageing brain.
CC   (Note: Revised entry submitted to correct the patent number format of
CC   US Government-owned NTIS applications to prevent clashes with ongoing US
CC   granted patent numbers. For further information please visit the Derwent
CC   web site at www.derwent.com/dwpi/updates/ntis_us.html.)
XX
SQ   Sequence 294 BP; 85 A; 63 C; 77 G; 69 T; 0 other;

  Query Match             22.0%;  Score 26.6;  DB 9;  Length 294;
  Best Local Similarity   58.0%;  Pred. No. 11;
  Matches   47;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy    11 TAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTG 70
         ||||  | |||  |      ||  ||   ||||||  ||   || || |  |||||||
Db   116 TAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCATTC 175

Qy    71 TTCGTTGTGTTATTAATGTTG 91
          || | ||||  |  | ||||
Db   176 ATCATGGTGTGGTGGAGGTTG 196


RESULT 33
AAQ88696
ID   AAQ88696 standard; cDNA to mRNA; 297 BP.
XX
AC   AAQ88696;
XX
DT   11-NOV-1995  (first entry)
XX
DE   Beta-amyloid precursor protein C-terminal peptide gene.
```

```
XX
KW   Human; beta-amyloid precursor protein; C-terminal peptide;
KW   gene transfer; transgenic animal; Alzheimer disease model;
KW   gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP653154-A.
XX
PD   17-MAY-1995.
XX
PF   07-NOV-1994;   94EP-0117512.
XX
PR   12-NOV-1993;   93JP-0306026.
XX
PA   (FARH ) HOECHST JAPAN LTD.
PA   (FARH ) HOECHST JAPAN KK.
XX
PI   Kawarabayashi T,  Kobayashi T,  Sato M,  Shoji M,  Tada N;
XX
DR   WPI; 1995-180492/24.
DR   P-PSDB; AAR74694.
XX
PT   Transgenic animal model for Alzheimer's disease - contains DNA encoding
PT   part of beta-amyloid precursor protein in a gene construct designed for
PT   over-expression in various cell types
XX
PS   Claim 2; Page 11; 32pp; English.
XX
CC   The sequence encodes a human brain beta-amyloid precursor protein
CC   (APP) C-terminal peptide.  The DNA may be transferred along with an
CC   APP signal peptide gene (e.g. AAQ88695) into somatic and germ cells of
CC   a non-human mammal, and the resulting transgenic animal may be used
CC   as a model for Alzheimer disease (AD).  The animal model exhibits
CC   symptoms similar to AD, producing large quantities of APP C-terminal
CC   peptide, death of neuron cells in pyrimidal cells at cerebral
CC   amyloid regions, increases in glial cells and deposition of
CC   abnormally phosphorylated tau protein.  The animal model may be
CC   used to develop new therapies for AD, including gene therapy
CC   strategies.
XX
SQ   Sequence 297 BP; 86 A; 64 C; 78 G; 69 T; 0 other;

  Query Match             22.0%;  Score 26.6;  DB 16;  Length 297;
  Best Local Similarity   58.0%;  Pred. No. 12;
  Matches   47;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy      11 TAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTG 70
           ||||  | |||  |      ||  ||   |||||||  ||   || || |  |||||||
Db     122 TAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCATTC 181

Qy      71 TTCGTTGTGTTATTAATGTTG 91
             || | ||||  |  | ||||
Db     182 ATCATGGTGTGGTGGAGGTTG 202


RESULT 34
AAQ88697
ID   AAQ88697 standard; cDNA to mRNA; 297 BP.
XX
AC   AAQ88697;
XX
DT   11-NOV-1995  (first entry)
XX
DE   Beta-amyloid precursor protein C-terminal peptide mutant gene.
XX
KW   Human; beta-amyloid precursor protein mutant; C-terminal peptide;
KW   gene transfer; transgenic animal; Alzheimer disease model;
KW   gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP653154-A.
XX
PD   17-MAY-1995.
XX
PF   07-NOV-1994;   94EP-0117512.
XX
PR   12-NOV-1993;   93JP-0306026.
XX
PA   (FARH ) HOECHST JAPAN LTD.
PA   (FARH ) HOECHST JAPAN KK.
XX
PI   Kawarabayashi T,  Kobayashi T,  Sato M,  Shoji M,  Tada N;
XX
DR   WPI; 1995-180492/24.
DR   P-PSDB; AAR74695.
XX
PT   Transgenic animal model for Alzheimer's disease - contains DNA encoding
PT   part of beta-amyloid precursor protein in a gene construct designed for
PT   over-expression in various cell types
XX
PS   Claim 2; Page 12-13; 32pp; English.
XX
CC   The sequence encodes a human brain beta-amyloid precursor protein
CC   (APP) mutant C-terminal peptide, and differs from AAQ88696 by a Glu
CC   to Gln conversion at codon-22.  The DNA may be transferred along
CC   with an APP signal peptide gene (e.g. AAQ88695) into somatic and germ
CC   cells of a non-human mammal, and the resulting transgenic animal may
CC   be used as a model for Alzheimer disease (AD).  The animal model
CC   exhibits symptoms similar to AD, producing large quantities of APP
CC   C-terminal peptide, death of neuron cells in pyrimidal cells at
CC   cerebral amyloid regions, increases in glial cells and deposition
CC   of abnormally phosphorylated tau protein.  The animal model may
CC   be used to develop new therapies for AD, including gene therapy
CC   strategies.
XX
SQ   Sequence 297 BP; 86 A; 65 C; 77 G; 69 T; 0 other;

  Query Match             22.0%;  Score 26.6;  DB 16;  Length 297;
  Best Local Similarity   58.0%;  Pred. No. 12;
  Matches   47;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy      11 TAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTG 70
           ||||  | |||  |      ||  ||   |||||||  ||   || || |  |||||||
Db     122 TAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCATTC 181

Qy      71 TTCGTTGTGTTATTAATGTTG 91
             || | ||||  |  | ||||
Db     182 ATCATGGTGTGGTGGAGGTTG 202


RESULT 35
AAQ42665
ID   AAQ42665 standard; cDNA; 300 BP.
XX
AC   AAQ42665;
XX
DT   27-OCT-1993  (first entry)
XX
DE   Full-length beta-amyloid protein coding region.
XX
KW   Alzheimer's Disease; Amyloid Plaque Core Protein; APCP;
KW   neuritic plaque; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..300
FT                   /*tag=  a
FT                   /product= beta-amyloid_protein
FT                   /note= "full-length coding sequence obtained by
FT                          combining overlapping clones SM2W3 and
FT                          SM2W4 (AAQ42664 and AAQ42663, respectively)"
FT   misc_difference 160..162
FT                   /*tag=  b
```

```
FT                   /codon= seq: AAC; aa: Lys
FT                   /note= "this codon is AAG in AAQ42664"
XX
PN   US5220013-A.
XX
PD   15-JUN-1993.
XX
PF   17-NOV-1986;   86US-0932193.
XX
PR   17-NOV-1986;   86US-0932193.
PR   31-DEC-1986;   86US-0948376.
PR   30-JAN-1987;   87US-0008810.
PR   18-AUG-1987;   87US-0087002.
PR   30-NOV-1989;   89US-0444118.
XX
PA   (SCIO-) SCIOS NOVA INC.
XX
PI   Cordell B,  Ponte PA;
XX
DR   WPI; 1993-205383/25.
DR   P-PSDB; AAR37866.
XX
PT   DNA sequence useful for detection of Alzheimer's disease - for
PT   encoding beta amyloid core protein
XX
PS   Disclosure; Fig 5; 40pp; English.
XX
CC   A clone was obtained from the genomic library described in Lawn et al.,
CC   Cell, 15:1157-1174 (1978) which included a 57 base pair segment which
CC   encodes amino acids 1-18 of the beta-amyloid protein, immediately
CC   preceded by a Methionine. A HindIII/RsaI fragment derived from the
CC   genomic clone and containing the 57bp segment was used to isolate cDNA
CC   fragments from a library prepared from temporal and parietal cortical
CC   tissue from a normal human brain. Lambda clone SM2W3 (AAQ42664) contains
CC   a 5' region segment which has a 6bp overlap with the 3' end of clone
CC   SM2W4 (AAQ42663). The full-length beta-amyloid protein coding sequence
CC   (AAQ42665), including an initiator Met residue which is probably
CC   processed in vivo, was obtained by combining the sequences of the
CC   two overlapping clones.
XX
SQ   Sequence 300 BP; 87 A; 65 C; 78 G; 70 T; 0 other;

  Query Match             22.0%;  Score 26.6;  DB 14;  Length 300;
  Best Local Similarity   58.0%;  Pred. No. 12;
  Matches   47;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy      11 TAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTG 70
           ||||  | |||  |      ||  ||   |||||||  ||   || || |  |||||||
Db     125 TAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAACAAGAAACAGTACACATCCATTC 184

Qy      71 TTCGTTGTGTTATTAATGTTG 91
           || | ||||  |  | ||||
Db     185 ATCATGGTGTGGTGGAGGTTG 205


RESULT 36
AAK99386
ID   AAK99386 standard; DNA; 300 BP.
XX
AC   AAK99386;
XX
DT   27-JUN-2002  (first entry)
XX
DE   DNA of wild type C99 portion of human APP.
XX
KW   Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta;
KW   amyloid precursor protein; tissue-specific expression control; human APP;
KW   APP pathway modulator; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200226820-A2.
XX
PD   04-APR-2002.
XX
PF   01-OCT-2001; 2001WO-EP11345.
XX
PR   29-SEP-2000; 2000US-236893P.
PR   14-JUN-2001; 2001US-298309P.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI   Cohen D,  Dengler UJ,  Finelli AL,  Freuler F,  Konsolaki M;
PI   Reinhardt MWHM,  Zusman S;
XX
DR   WPI; 2002-315796/35.
XX
PT   New transgenic fly, containing DNA encoding an Abeta portion of human
PT   APP, useful for identifying agents which modulate the APP pathway and
PT   which can be used to treat Alzheimer's disease -
XX
PS   Claim 4; Page 84; 129pp; English.
XX
CC   The invention relates to a transgenic fly whose genome comprises DNA
CC   encoding a polypeptide having the Abeta portion of human amyloid
CC   precursor protein (APP), fused to a signal sequence. The DNA sequence
CC   encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
CC   the specification. The DNA sequence is operably linked to a tissue-
CC   specific expression control sequence. Expression of the sequence gives
CC   the fly an altered phenotype. The purpose of the invention is for
CC   identifying agents that inhibit or promote the expression and/or function
CC   of genes or encoded polypeptides which modify the APP pathway. The agent
CC   is a compound, triple helix DNA, antisense oligonucleotide, double
CC   stranded RNA molecule, ribozyme, or particularly an antibody. It is used
CC   to treat conditions such as Alzheimer's disease. The agent can be used as
CC   an APP pathway modulator or in gene therapy. This polynucleotide sequence
CC   represents the DNA of the wild type C99 portion of human APP of the
CC   invention.
XX
SQ   Sequence 300 BP; 87 A; 65 C; 79 G; 69 T; 0 other;

  Query Match             22.0%;  Score 26.6;  DB 24;  Length 300;
  Best Local Similarity   58.0%;  Pred. No. 12;
  Matches   47;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy      11 TAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTG 70
           ||||  | |||  |      ||  ||   |||||||  ||   || || |  |||||||
Db     122 TAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCATTC 181

Qy      71 TTCGTTGTGTTATTAATGTTG 91
           || | ||||  |  | ||||
Db     182 ATCATGGTGTGGTGGAGGTTG 202


RESULT 37
AAA39488
ID   AAA39488 standard; DNA; 303 BP.
XX
AC   AAA39488;
XX
DT   24-AUG-2000  (first entry)
XX
DE   Human APP C100 DNA fragment.
XX
KW   APP; amyloid precursor protein; C100; transgene; Alzheimer's disease;
KW   gamma-secretase; alpha-secretase; ss.
XX
OS   Homo sapiens.
XX
PN   DE19849073-A1.
XX
PD   27-APR-2000.
XX
PF   24-OCT-1998;   98DE-1049073.
XX
```

```
PR   24-OCT-1998;   98DE-1049073.
XX
PA   (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI   Peraus G,  Hoppe E,  Baumeister R;
XX
DR   WPI; 2000-304753/27.
XX
PT   Transgene encoding amyloid precursor protein or its fragment, used to
PT   produce transgenic nematodes used, e.g. to screen for agents for
PT   treating Alzheimer's disease  -
XX
PS   Claim 3; Page 6; 16pp; German.
XX
CC   This invention describes a novel transgene (I) which comprises (i) a
CC   sequence (Ia) that encodes either the complete amyloid precursor protein
CC   (APP) or a part of its Abeta peptide (AbP), but is not identical with
CC   the part of the APP sequence that encodes the complete AbP; (ii)
CC   optionally one or more additional coding and/or non-coding sequences and
CC   (iii) a promoter functional in Caenorhabditis elegans. Cleavage of APP
CC   by alpha-secretase does not lead to AbP, but cleavage with beta or
CC   gamma-secretases does, so modulation of these activities is used to
CC   reduce the amount of AbP, a major component of the plaque found in
CC   Alzheimer patients, produced. (I), or expression vectors containing it,
CC   are used to produce transgenic cells (optionally part of a non-human
CC   animal), specifically C. elegans. The transgenic animals are used (i) to
CC   identify gamma and/or alpha-secretase activities in C. elegans; (ii) to
CC   identify/or characterize substances that inhibit gamma-secretase or
CC   increase alpha-secretase activities, or (iii) to identify and/or
CC   characterize agents potentially useful for treatment or prevention of
CC   Alzheimer's disease. This sequence represents the human APP protein C100
CC   fragment which is used in the construction of the transgene described in
CC   the method of the invention.
XX
SQ   Sequence 303 BP; 87 A; 65 C; 80 G; 71 T; 0 other;

  Query Match             22.0%;  Score 26.6;  DB 21;  Length 303;
  Best Local Similarity   58.0%;  Pred. No. 12;
  Matches   47;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy      11 TAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTG 70
           ||||  | |||  |       ||  ||   |||||||  ||    || || |  |||||||
Db     125 TAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCATTC 184

Qy      71 TTCGTTGTGTTATTAATGTTG 91
             || | ||||  |  | ||||
Db     185 ATCATGGTGTGGTGGAGGTTG 205


RESULT 38
AAQ88699
ID   AAQ88699 standard; cDNA to mRNA; 309 BP.
XX
AC   AAQ88699;
XX
DT   11-NOV-1995  (first entry)
XX
DE   Beta-amyloid precursor protein C-terminal peptide gene.
XX
KW   Human; beta-amyloid precursor protein; C-terminal peptide;
KW   gene transfer; transgenic animal; Alzheimer disease model;
KW   gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP653154-A.
XX
PD   17-MAY-1995.
XX
PF   07-NOV-1994;   94EP-0117512.
XX
PR   12-NOV-1993;   93JP-0306026.
XX
PA   (FARH ) HOECHST JAPAN LTD.
PA   (FARH ) HOECHST JAPAN KK.
XX
PI   Kawarabayashi T,  Kobayashi T,  Sato M,  Shoji M,  Tada N;
XX
DR   WPI; 1995-180492/24.
DR   P-PSDB; AAR74697.
XX
PT   Transgenic animal model for Alzheimer's disease - contains DNA encoding
PT   part of beta-amyloid precursor protein in a gene construct designed for
PT   over-expression in various cell types
XX
PS   Claim 2; Page 15; 32pp; English.
XX
CC   The sequence encodes a human brain beta-amyloid precursor protein
CC   (APP) C-terminal peptide.  The DNA may be transferred along with an
CC   APP signal peptide gene (e.g. AAQ88695) into somatic and germ cells
CC   of a non-human mammal, and the resulting transgenic animal may be
CC   used as a model for Alzheimer disease (AD).  The animal model
CC   exhibits symptoms similar to AD, producing large quantities of APP
CC   C-terminal peptide, death of neuron cells in pyrimidal cells at
CC   cerebral amyloid regions, increases in glial cells and deposition
CC   of abnormally phosphorylated tau protein.  The animal model may
CC   be used to develop new therapies for AD, including gene therapy
CC   strategies.
XX
SQ   Sequence 309 BP; 91 A; 64 C; 83 G; 71 T; 0 other;

  Query Match             22.0%;  Score 26.6;  DB 16;  Length 309;
  Best Local Similarity   58.0%;  Pred. No. 12;
  Matches   47;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy      11 TAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTG 70
           ||||  | |||  |       ||  ||   |||||||  ||    || || |  |||||||
Db     134 TAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCATTC 193

Qy      71 TTCGTTGTGTTATTAATGTTG 91
             || | ||||  |  | ||||
Db     194 ATCATGGTGTGGTGGAGGTTG 214


RESULT 39
AAQ88700
ID   AAQ88700 standard; cDNA to mRNA; 309 BP.
XX
AC   AAQ88700;
XX
DT   11-NOV-1995  (first entry)
XX
DE   Beta-amyloid precursor protein C-terminal peptide mutant gene.
XX
KW   Human; beta-amyloid precursor protein mutant; C-terminal peptide;
KW   gene transfer; transgenic animal; Alzheimer disease model;
KW   gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP653154-A.
XX
PD   17-MAY-1995.
XX
PF   07-NOV-1994;   94EP-0117512.
XX
PR   12-NOV-1993;   93JP-0306026.
XX
PA   (FARH ) HOECHST JAPAN LTD.
PA   (FARH ) HOECHST JAPAN KK.
XX
PI   Kawarabayashi T,  Kobayashi T,  Sato M,  Shoji M,  Tada N;
XX
DR   WPI; 1995-180492/24.
DR   P-PSDB; AAR74698.
XX
```

```
PT   Transgenic animal model for Alzheimer's disease - contains DNA encoding
PT   part of beta=amyloid precursor protein in a gene construct designed for
PT   over-expression in various cell types
XX
PS   Claim 2; Page 16-17; 32pp; English.
XX
CC   The sequence encodes a human brain beta-amyloid precursor protein
CC   (APP) mutant C-terminal peptide, and differs from AAQ88699 by
CC   conversion of Lys to Asn at codon-3 and Met to Leu at codon-4.  The
CC   DNA may be transferred along with an APP signal peptide gene (e.g.
CC   AAQ88695) into somatic and germ cells of a non-human mammal, and the
CC   resulting transgenic animal may be used as a model for Alzheimer
CC   disease (AD).  The animal model exhibits symptoms similar to AD,
CC   producing large quantities of APP C-terminal peptide, death of
CC   neuron cells in pyrimidal cells at cerebral amyloid regions,
CC   increases in glial cells and deposition of abnormally
CC   phosphorylated tau protein.  The animal model may be used to develop
CC   new therapies for AD, including gene therapy strategies.
XX
SQ   Sequence 309 BP; 90 A; 65 C; 82 G; 72 T; 0 other;

  Query Match             22.0%;  Score 26.6;  DB 16;  Length 309;
  Best Local Similarity   58.0%;  Pred. No. 12;
  Matches   47;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy      11 TAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTG 70
           ||||  | |||  |      ||  ||   ||||||| ||   || || |  |||||||
Db     134 TAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCATTC 193

Qy      71 TTCGTTGTGTTATTAATGTTG 91
              || | ||||  |  | ||||
Db     194 ATCATGGTGTGGTGGAGGTTG 214


RESULT 40
AAD20982
ID   AAD20982 standard; DNA; 315 BP.
XX
AC   AAD20982;
XX
DT   15-JAN-2002  (first entry)
XX
DE   Human recombinant beta-amyloid precursor protein (betaAPP) C-83 DNA.
XX
KW   Human; Alzheimer's disease; gamma-secretase; integral-membrane protein;
KW   beta-amyloid precursor protein; betaAPP; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..315
FT                   /*tag=  a
FT                   /product= "Human recombinant betaAPP protein (C-83)"
XX
PN   WO200175435-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US10453.
XX
PR   03-APR-2000; 2000US-194495P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Roberts SB,  Hendrick JP,  Vinitsky A,  Lewis M,  Smith DW,  Pak R;
XX
DR   WPI; 2001-648575/74.
DR   P-PSDB; AAE12897.
XX
PT   Novel gamma secretase protein, useful in the production of amyloids, is
PT   capable of cleaving beta-amyloid precursor protein to produce beta
PT   amyloid peptide -
XX
PS   Example 1; Fig 3; 127pp; English.
XX
CC   The invention relates to the field of plaque amyloid deposits that are
CC   the hallmarks of Alzheimer's disease. In particular, the invention
CC   relates to an isolated, functionally-active protein that has
CC   gamma-secretase activity. Gamma-secretase activity is necessary for
CC   amyloid production. The present invention also relates to methods for
CC   isolating integral-membrane proteins and protein complexes, including
CC   the gamma-secretase protein of the invention. The method is useful for
CC   monitoring the cleavage of beta-amyloid precursor protein (betaAPP)
CC   by gamma-secretase. The present sequence is a DNA encoding human
CC   recombinant betaAPP protein (C-83).
XX
SQ   Sequence 315 BP; 75 A; 75 C; 92 G; 73 T; 0 other;

  Query Match             22.0%;  Score 26.6;  DB 22;  Length 315;
  Best Local Similarity   58.0%;  Pred. No. 12;
  Matches   47;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy      11 TAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTG 70
           ||||  | |||  |      ||  ||   ||||||| ||   || || |  |||||||
Db     137 TAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCATTC 196

Qy      71 TTCGTTGTGTTATTAATGTTG 91
              || | ||||  |  | ||||
Db     197 ATCATGGTGTGGTGGAGGTTG 217


RESULT 41
AAD23935
ID   AAD23935 standard; DNA; 327 BP.
XX
AC   AAD23935;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Gamma-secretase substrate #1 DNA.
XX
KW   Gamma-secretase substrate; beta-CTF domain; amyloid precursor protein;
KW   APP; beta-secretase; Alzheimer's disease; fusion protein; ds.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..327
FT                   /*tag=  a
FT                   /product= "Gamma-secretase substrate"
FT                   /note= "This substrate contains APP beta-CTF domain and
FT                   hydrophilic moiety fusion"
FT   misc_feature    1..300
FT                   /*tag=  b
FT                   /note= "APP beta-CTF domain DNA"
FT   misc_feature    301..324
FT                   /*tag=  c
FT                   /note= "Region encoding hydrophilic moiety"
XX
PN   WO200183811-A1.
XX
PD   08-NOV-2001.
XX
PF   25-APR-2001; 2001WO-US13332.
XX
PR   01-MAY-2000; 2000US-201053P.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Li Y,  Xu M,  Huang Q,  Gardell S;
XX
DR   WPI; 2002-066536/09.
DR   P-PSDB; AAE14379.
XX
PT   Novel gamma secretase substrate for assaying gamma secretase activity
PT   and identifying compounds that regulate gamma secretase activity, e.g.
```

```
PT   inhibitors of gamma secretase useful for treating Alzheimer's disease
PT   -
XX
PS   Example 1; Page 12-13; 36pp; English.
XX
CC   The invention relates to gamma-secretase substrates containing
CC   a hydrophilic polypeptide moiety covalently joined to the carboxyl
CC   terminus of a beta-CTF domain. A beta-CTF domain is a polypeptide that
CC   can be cleaved by gamma-secretase, and that approximates the
CC   C-terminal fragment (amino acids 596-695) of amyloid precursor protein
CC   (APP) produced after cleavage of APP by beta-secretase. The
CC   hydrophilic polypeptide moiety increases the solubility of the
CC   substrate in a zwitterionic detergent. The gamma-secretase substrate
CC   is used in in vitro assays employing zwitterionic detergent for
CC   measuring gamma-secretase activity. The assay methods are useful for
CC   purifying and characterising the enzyme, to screen for compounds that
CC   modulate gamma-secretase activity, and to test the ability of a
CC   particular compound that affect gamma-secretase activity. The compounds
CC   that modulate gamma-secretase activity include gamma-secretase
CC   inhibitors which are useful in the treatment of Alzheimer's disease,
CC   and in the characterisation of the biological importance of
CC   gamma-secretase. The present sequence is a DNA encoding gamma-secretase
CC   substrate of the invention. The substrate is a fusion protein
CC   containing APP beta-CTF domain and a hydrophilic moiety.
XX
SQ   Sequence 327 BP; 100 A; 68 C; 85 G; 74 T; 0 other;

  Query Match             22.0%;  Score 26.6;  DB 24;  Length 327;
  Best Local Similarity   58.0%;  Pred. No. 12;
  Matches   47;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy      11 TAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTG 70
           ||||  | |||  |       ||  ||   |||||||  ||   || || |  |||||||
Db     125 TAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCATTC 184

Qy      71 TTCGTTGTGTTATTAATGTTG 91
              || | ||||  |  | ||||
Db     185 ATCATGGTGTGGTGGAGGTTG 205


RESULT 42
AAT18082
ID   AAT18082 standard; DNA; 336 BP.
XX
AC   AAT18082;
XX
DT   10-OCT-1996  (first entry)
XX
DE   Familial Alzheimer's disease APP isoform 751 gene fragment.
XX
KW   APP; amyloid precursor protein; isoform 751; inherent; familial;
KW   Alzheimer's disease; mutation; diagnosis; transgenic model; study;
KW   cognitive; beta A4 domain; exon 17; senility; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Exon            1..336
FT                   /*tag=  a
FT                   /number= 17
FT                   /transl_except= pos: 175-177, aa: Ile
FT                   /note= "encodes amino acids 640-751 of full APP
FT                          isoform 751, the translation exception
FT                          at posn. 175-177 is the site of a Val to
FT                          Ile mutation in isoform 751, bases 175-177
FT                          probably should be ATC and not TTC"
FT   misc_feature    43..168
FT                   /*tag=  b
FT                   /note= "encodes the beta-A4 domain"
XX
PN   WO9606927-A1.
XX
PD   07-MAR-1996.
XX
PF   28-AUG-1995;   95WO-US10920.
XX
PR   01-SEP-1994;   94US-0299872.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Chen HY,  Heavens RP,  Singh G,  Sirinathsinghji DJS;
PI   Smith DW,  Trumbauer ME,  Van Der Ploeg LHT,  Vongs A;
PI   Zheng H;
XX
DR   WPI; 1996-160358/16.
DR   P-PSDB; AAR93556.
XX
PT   Transgenic animal expressing familial form of human amyloid
PT   precursor protein  - used to evaluate compounds affecting
PT   Alzheimer's disease and other cognitive disorders
XX
PS   Example 1; Fig 7; 32pp; English.
XX
CC   AAT18082 represents exon 17 of the amyloid precursor protein (APP)
CC   isoform 751 gene from a patient diagnosed with familial Alzheimer's
CC   disease (FAD). The sequence given corresponds to the coding sequence
CC   for amino acids 640-751 of FAD APP 751. A feature of FAD is a Val to
CC   Ile substitution at posn. 698 of the full APP (encoded by bases 175
CC   to 177 of this sequence). DNA encoding this sequence was used to
CC   construct expression vectors for the prodn. of transgenic animals (esp.
CC   mice) carrying the FAD APP 751 mutation. The transgenic animals are
CC   useful for the evaluation of test cpds. affecting Alzheimer's disease
CC   and other cognitive disorders and for identification of new targets
CC   in Alzheimer's disease since the progression of the disease can be
CC   followed gradually.
CC   N.B. the V-I mutation encoded at base 175-177, is given in the
CC   specification as a TTC codon (most probably this should be ATC).
XX
SQ   Sequence 336 BP; 102 A; 69 C; 88 G; 77 T; 0 other;

  Query Match             22.0%;  Score 26.6;  DB 17;  Length 336;
  Best Local Similarity   58.0%;  Pred. No. 12;
  Matches   47;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy      11 TAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTG 70
           ||||  | |||  |       ||  ||   |||||||  ||   || || |  |||||||
Db     161 TAGCGACAGTGATCTTCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCATTC 220

Qy      71 TTCGTTGTGTTATTAATGTTG 91
              || | ||||  |  | ||||
Db     221 ATCATGGTGTGGTGGAGGTTG 241


RESULT 43
AAQ59415
ID   AAQ59415 standard; cDNA; 337 BP.
XX
AC   AAQ59415;
XX
DT   16-MAR-1994  (first entry)
XX
DE   Human brain Expressed Sequence Tag EST00434.
XX
KW   Gene transcription product; genetic markers; tagging; in vivo;
KW   transcription; mapping; locations; chromosomes; chromosomal; ss.
XX
OS   Homo sapiens.
XX
PN   WO9316178-A.
XX
PD   19-AUG-1993.
XX
PF   12-FEB-1993;   93WO-US01294.
XX
PR   12-FEB-1992;   92US-0837195.
XX
```

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PA   (USSH ) US DEPT HEALTH & HUMAN SERVICE.
XX
PI   Adams MD,  Moreno RF,  Venter CJ;
XX
DR   WPI; 1993-272882/34.
XX
PT   Enriched oligonucleotides and corresp. sequences - used as
PT   markers for human genes transcribed in-vivo, facilitate tagging
PT   of most human genes
XX
PS   Example 4; Page 171; 500pp; English.
XX
CC   The Expressed Sequence Tag was isolated from a human brain cDNA
CC   library as part of a large set of ESTs which can be used as markers
CC   for human genes transcribed in vivo. They can be used to facilitate
CC   tagging of most human genes, for mapping locations of expressed genes
CC   on chromosomes, for individual or forensic identification, for mapping
CC   locations of disease-associated genes, for identification of tissue
CC   type, and for prepn. of antisense sequences, probes and constructs.
CC   EST00434 has a "poor" coding probability as evaluated using the
CC   coding-region prediction program CRM. See also AAQ59041-Q61440.
XX
SQ   Sequence 337 BP; 95 A; 63 C; 66 G; 107 T; 6 other;

  Query Match             22.0%;  Score 26.6;  DB 14;  Length 337;
  Best Local Similarity   54.9%;  Pred. No. 12;
  Matches   50;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy      11 TAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTG 70
           |  | | ||    | ||    | ||  ||    | ||||||          | ||||||||
Db      58 TNACTTAGGCTTTCTGAGACTCACTTTCCTCCTTTATAAATCAGGAAGAATAATCCATTG 117

Qy      71 TTCGTTGTGTTATTAATGTTGTATAATTGAG 101
             || ||| ||| |||||     |||| ||||
Db     118 CTCATTGAGTTGTTAATNAGACATAAATGAG 148


RESULT 44
AAV07188
ID   AAV07188 standard; DNA; 354 BP.
XX
AC   AAV07188;
XX
DT   09-SEP-1998  (first entry)
XX
DE   Flag-amyloid protein precursor (FLAG-APP-C100) fusion protein.
XX
KW   Amyloid protein precursor; APP-C100; fusion protein; FLAG-APP-C100;
KW   transgenic animal; Alzheimer's disease; mouse; neurodegeneration;
KW   brain; ss.
XX
OS   Chimeric - Synthetic.
OS   Chimeric - Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..351
FT                   /*tag=  a
FT                   /product= "FLAG-APP-C100"
FT                   /note= "no start or stop codon specified"
XX
PN   WO9816627-A1.
XX
PD   23-APR-1998.
XX
PF   16-OCT-1997;   97WO-US18202.
XX
PR   16-OCT-1996;   96US-0729345.
XX
PA   (MCLE-) MCLEAN HOSPITAL CORP.
PA   (WELL-) WELLESLEY COLLEGE.
XX
PI   Berger-Sweeney J,  Neve RL;
XX
DR   WPI; 1998-251279/22.
DR   P-PSDB; AAW51102.
XX
PT   Transgenic animal with rapid development of Alzheimer disease
PT   characteristics - contains nucleic acid encoding fragment of amyloid
PT   protein precursor fused to Flag peptide, useful as model for
PT   screening potential therapeutic agents
XX
PS   Claim 5; Pages 26-27; 41pp; English.
XX
CC   This is the nucleotide sequence of the FLAG-Amyloid protein precursor
CC   (FLAG-APP-C100), used in the method of the invention, involving the
CC   creation of an FLAG-amyloid protein precursor fusion protein, as well
CC   as a transgenic animal with rapid development of Alzheimer's disease.
CC   The animals, specifically mice, show increased neurodegeneration in the
CC   brain and cognitive impairment, so are used as in vivo models for
CC   screening agents potentially useful in treatment of Alzheimer's disease.
XX
SQ   Sequence 354 BP; 107 A; 71 C; 95 G; 81 T; 0 other;

  Query Match             22.0%;  Score 26.6;  DB 19;  Length 354;
  Best Local Similarity   58.0%;  Pred. No. 12;
  Matches   47;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy      11 TAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTG 70
           ||||  | |||  |      ||  ||   |||||||  ||   || || |  |||||||
Db     176 TAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCATTC 235

Qy      71 TTCGTTGTGTTATTAATGTTG 91
             || | ||||  |   | ||||
Db     236 ATCATGGTGTGGTGGAGGTTG 256


RESULT 45
AAV20379
ID   AAV20379 standard; DNA; 354 BP.
XX
AC   AAV20379;
XX
DT   26-JUN-1998  (first entry)
XX
DE   DNA for APP C-terminal fragment mutant SPA4CT Thr43Phe.
XX
KW   Human; amyloid precursor protein; APP; carboxy-terminal fragment;
KW   A4CT; mutant SPA4CT Thr43Phe; disease model; treatment;
KW   Alzheimer's disease; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..354
FT                   /*tag=  a
FT                   /note= "stop codon not given"
XX
PN   WO9803643-A2.
XX
PD   29-JAN-1998.
XX
PF   17-JUL-1997;   97WO-EP03960.
XX
PR   08-MAY-1997;   97GB-0009239.
PR   22-JUL-1996;   96GB-0015351.
PR   09-SEP-1996;   96GB-0018804.
XX
PA   (SMIK ) SMITHKLINE BEECHAM AUSTRALIA PTY LTD.
PA   (SMIK ) SMITHKLINE BEECHAM PHARMA GMBH.
XX
PI   Beyreuther K,  Lichtenthaler S,  Masters CL,  Prior P;
XX
DR   WPI; 1998-120768/11.
DR   P-PSDB; AAW50029.
XX
```

PT Construct containing sequence for mutant form of amyloid precursor
PT protein - or its C-terminal fragment, and related transgenic animals
PT or transformed cells, used for identifying potential drugs for
PT Alzheimer's disease
XX
PS Claim 10; Page 10; 15pp; English.
XX
CC The present sequence encodes the human amyloid precursor protein
CC (APP) C-terminal fragment (A4CT) mutant SPA4CT Thr43Phe.
CC The mutation results in a higher ratio of beta A4 1-42 to beta A4
CC 1-40, useful in disease models to identify potential drugs for the
CC treatment of Alzheimer's disease.
XX
SQ Sequence 354 BP; 89 A; 83 C; 99 G; 83 T; 0 other;

Query Match 22.0%; Score 26.6; DB 19; Length 354;
Best Local Similarity 58.0%; Pred. No. 12;
Matches 47; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

```
Qy      11 TAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTG 70
           |||| |  |||  |      ||  ||   |||||||  ||   || || |  |||||||
Db     179 TAGCATTCGTGATCGTCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCATTC 238

Qy      71 TTCGTTGTGTTATTAATGTTG 91
             || | ||||  |  | ||||
Db     239 ATCATGGTGTGGTGGAGGTTG 259
```

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GenCore version 5.1.4_p5_4578

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Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	61	28.4	877	2	AC2211	heme transport pro
c	2	58.5	27.1	155	2	H89787	hypothetical prote
	3	58	27.0	472	2	G75298	ribosomal protein
c	4	56	25.9	701	2	T17243	hypothetical prote
c	5	55	25.5	86	2	T31059	hypothetical prote
	6	55	25.6	365	2	T29224	hypothetical prote
	7	55	25.6	881	1	RGBYG4	regulatory protein
c	8	54.5	25.2	2110	2	B44110	mycocerosate synth
c	9	54.5	25.2	2111	2	A70668	mycocerosate synth
c	10	54.5	25.2	2116	2	C86926	probable mycoceros
c	11	54	25.0	382	1	S22652	transcription fact
	12	54	25.1	616	2	T08708	hypothetical prote
c	13	54	25.0	737	2	T15597	hypothetical prote
c	14	54	25.0	849	2	T22306	hypothetical prote
c	15	54	25.0	1017	2	T15598	hypothetical prote
c	16	53.5	24.8	1174	2	T49868	related to suppres
	17	53	24.7	134	2	A87423	hypothetical prote
c	18	53	24.5	302	2	F90445	conserved hypothet
	19	53	24.7	400	2	B69081	acetyl-CoA synthet
c	20	53	24.5	928	2	T24868	hypothetical prote
c	21	53	24.5	1844	2	D71612	hypothetical prote
c	22	53	24.5	2715	2	T13049	eyelid - fruit fly
c	23	52	24.1	388	2	G95375	probable drug resi
	24	52	24.2	451	2	G83916	glycolate oxidase
c	25	52	24.1	763	2	S17998	gene COX1 intron 4
	26	52	24.2	1091	2	C75585	carboxylase - Dein
c	27	51.5	23.8	627	2	S48424	hypothetical prote
c	28	51.5	23.8	1469	2	T24216	chromosome condens
c	29	51.5	23.8	2126	2	E70522	probable polyketid
	30	51	23.7	371	2	T04971	hypothetical prote
	31	51	23.7	399	2	T47873	phosphatidate cyti
	32	51	23.7	433	2	T32605	hypothetical prote
c	33	51	23.6	559	1	JQ2010	transcription fact
	34	51	23.7	884	2	T18649	hypothetical prote
c	35	51	23.6	885	2	I38968	100 kDa coactivato
c	36	51	23.6	922	2	F81539	polymorphic membra
c	37	51	23.6	922	2	B72131	polymorphic outer
c	38	51	23.6	922	2	E86491	polymorphic outer
c	39	51	23.6	1672	2	T46237	hypothetical prote
c	40	50.5	23.4	74	2	T18144	hypothetical prote
	41	50.5	23.5	179	2	AD1012	conserved hypothet
c	42	50.5	23.4	259	2	T49596	related to H+-tran
c	43	50.5	23.4	330	2	B97980	dihydroorotate oxi
c	44	50.5	23.4	415	2	S39535	corticotropin-rele
c	45	50.5	23.4	415	2	I58144	corticotropin-rele
c	46	50.5	23.4	444	2	A48260	corticoliberin rec
c	47	50.5	23.4	534	2	S31300	regulatory protein
c	48	50.5	23.4	550	2	A64826	hybrid cluster [4F
c	49	50.5	23.4	550	2	AI0608	prismane protein h
c	50	50.5	23.4	552	2	G90748	probable prismane

ALIGNMENTS

RESULT 1
AC2211
heme transport protein alr3242 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AC2211
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC2211
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-877 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74941.1; PID:g17132337; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr3242

Alignment Scores:

Pred. No.:	1.57	Length:	877
Score:	61.00	Matches:	13
Percent Similarity:	55.56%	Conservative:	7
Best Local Similarity:	36.11%	Mismatches:	16
Query Match:	28.37%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_1_121 (1-121) x AC2211 (1-877)

Qy 12 AGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGT 71

```
Db    412 SerLeuGlyTyrGlnTyrAspAsnProAsnSerLysSerTrpLeuGlnPheValArgAla 431

Qy     72 TCGTTGTGTTATTAATGTTGTATAATTGAGCAGGACACAACACGTACG 119
          :::|||   |||         |||||||||:::|||:::   |||:::
Db    432 AsnLeuTyrTyrGlnAsnAlaIleIleGluGluAspSerAsnArgSer 447
```

RESULT 2
H89787
hypothetical protein SA0236 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: H89787
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: H89787
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-155 <KUR>
A;Cross-references: GB:BA000018; PID:g13700160; PIDN:BAB41459.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA0236

Alignment Scores:

Pred. No.:	3.65	Length:	155
Score:	58.50	Matches:	14
Percent Similarity:	57.14%	Conservative:	10
Best Local Similarity:	33.33%	Mismatches:	11
Query Match:	27.08%	Indels:	7
DB:	2	Gaps:	2

US-09-198-779B-1_COPY_1_121 (1-121) x H89787 (1-155)

```
Qy    113 TGTTGTGTCCTGCTCAATTATACAACATTA------ATAACACAACGAACA--------- 69
          |||   |||   :::   :::|||   :::      |||      ||||||
Db     61 CysSerValAlaIleProHisThrAspValGluHisIleAsnHisArgThrIleGlyVal 80

Qy     68 ------ATGGATCAGGACCGTCCATTTATCAGCATGGGCAGCGTCGATCTGTCCACCGAG 15
                :::::::::::   |||||||||   ||||||::::::|||      ||||||
Db     81 AlaValLeuGluLysGluValProPheIleGluMetGlyThrLeuAspGlnGlnThrGlu 100

Qy     14 GCTAGA 9
             :::
Db    101 ValLys 102
```

RESULT 3
G75298
ribosomal protein S2-related protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C;Accession: G75298
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G75298
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-472 <WHI>
A;Cross-references: GB:AE002056; GB:AE000513; NID:g6460037; PIDN:AAF11786.1; PID:g646004
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR2241
A;Map position: 1
C;Superfamily: Deinococcus radiodurans hypothetical protein DRA0012

Alignment Scores:

Pred. No.:	4.41	Length:	472
Score:	58.00	Matches:	10
Percent Similarity:	64.71%	Conservative:	1
Best Local Similarity:	58.82%	Mismatches:	6
Query Match:	26.98%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_1_121 (1-121) x G75298 (1-472)

```
Qy     18 GGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCAT 68
          ||||||   ||||||   ||||||||||:::   |||      |||   |||
Db    268 GlyGlyAspIleAspGlnAlaHisAlaGluAlaTrpAlaAlaLeuArgHis 284
```

RESULT 4
T17243
hypothetical protein DKFZp586B0217.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17243
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18722
A;Accession: T17243
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-701 <KOE>
A;Cross-references: EMBL:AL117449
A;Experimental source: adult uterus; clone DKFZp586B0217
C;Genetics:
A;Note: DKFZp586B0217.1

Alignment Scores:

Pred. No.:	8.87	Length:	701
Score:	56.00	Matches:	14
Percent Similarity:	52.63%	Conservative:	6
Best Local Similarity:	36.84%	Mismatches:	10
Query Match:	25.93%	Indels:	8
DB:	2	Gaps:	1

US-09-198-779B-1_COPY_1_121 (1-121) x T17243 (1-701)

```
Qy    104 CTGCTCAATTATACAACATTAATAACACAACGAACAATGGATCAGGACCGT--------- 54
          |||   |||:::   ||||||:::||||||||||||:::|||:::::
Db    302 LeuLysAsnPheTyrThrLeuValThrGlnArgThrLeuAspArgGluSerGlnAlaGlu 321

Qy     53 ---------------CCATTTATCAGCATGGGCAGCGTCGATCTGTCCACCGAG 15
                                  ||||||:::      |||   ||||||
Db    322 TyrAsnIleThrIleThrValThrAspMetGlyThrProArgLeuLysThrGlu 339
```

RESULT 5
T31059
hypothetical protein C05D9.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 29-Oct-1999
C;Accession: T31059
R;Fulton, L.; Gattung, S.
submitted to the EMBL Data Library, September 1999
A;Description: The sequence of C. elegans cosmid C05D9.
A;Reference number: Z20960
A;Accession: T31059
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-86 <FUL>
A;Cross-references: EMBL:U64605; PIDN:AAB04585.1
A;Experimental source: strain Bristol N2
C;Genetics:
A;Map position: X
A;Introns: 19/1; 53/3
A;Note: C05D9.4

Alignment Scores:

Pred. No.:	12.2	Length:	86
Score:	55.00	Matches:	12

```
Percent Similarity:     44.44%          Conservative:  4
Best Local Similarity:  33.33%          Mismatches:    20
Query Match:            25.46%          Indels:        0
DB:                     2               Gaps:          0

US-09-198-779B-1_COPY_1_121 (1-121) x T31059 (1-86)

Qy    120 ACGTACGTGTTGTGTCCTGCTCAATTATACAACATTAATAACACAACGAACAATGGATCA 61
          ||||||                  :::|||   |||               |||   :::
Db     20 ThrTyrSerThrTyrHisGlyAsnIleTyrGlyIleGlnLysLeuLysGlyAsnLysThr 39

Qy     60 GGACCGTCCATTTATCAGCATGGGCAGCGTCGATCTGTCCACCGAGGC 13
          |||   |||:::|||||||||         :::      |||   |||
Db     40 GlyLysSerValTyrGlnHisPheTrpPheLysArgHisHisLeuGly 55

RESULT 6
T29224
hypothetical protein F55G1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29224
R;Murray, J.; Le, T.T.
submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid F55G1.
A;Reference number: Z20591
A;Accession: T29224
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-365 <MUR>
A;Cross-references: EMBL:U58750; PIDN:AAB00643.1; GSPDB:GN00022; CESP:F55G1.6
A;Experimental source: strain Bristol N2; clone F55G1
C;Genetics:
A;Gene: CESP:F55G1.6
A;Map position: 4
A;Introns: 28/3; 63/2; 241/1

Alignment Scores:
Pred. No.:              12.4            Length:        365
Score:                  55.00           Matches:       11
Percent Similarity:     53.57%          Conservative:  4
Best Local Similarity:  39.29%          Mismatches:    11
Query Match:            25.58%          Indels:        2
DB:                     2               Gaps:          1

US-09-198-779B-1_COPY_1_121 (1-121) x T29224 (1-365)

Qy      6 CCGTCTAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGAT------AAATGGACGGTC 59
          |||          |||   :::   :::|||      |||      |||:::   |||
Db     16 ProAspAspThrHisGlyAspValArgSerAlaSerGluAspAlaThrLysPheProVal 35

Qy     60 CTGATCCATTGTTCGTTGTGTTAT 83
               |||||||||   :::||||||
Db     36 AlaIleHisCysHisIleCysTyr 43

RESULT 7
RGBYG4
regulatory protein GAL4 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein P1021; protein YPL248c
C;Species: Saccharomyces cerevisiae
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jul-2000
C;Accession: A05022; S61016; S65277; S12977
R;Laughon, A.; Gesteland, R.F.
Mol. Cell. Biol. 4, 260-267, 1984
A;Title: Primary structure of the Saccharomyces cerevisiae GAL4 gene.
A;Reference number: A05022; MUID:84141879; PMID:6366516
A;Accession: A05022
A;Molecule type: DNA
A;Residues: 1-881 <LAU>
A;Cross-references: EMBL:K01486; NID:g171557; PIDN:AAA34626.1; PID:g171558
R;Gadhavi, P.L.; Raine, A.R.C.; Alefounder, P.R.; Laue, E.D.
FEBS Lett. 276, 49-53, 1990
A;Title: Complete assignment of the (1)H NMR spectrum and secondary structure of the DNA
A;Reference number: S12977; MUID:91092433; PMID:2265711
A;Contents: annotation; zinc finger
R;Pohl, T.M.
submitted to the EMBL Data Library, November 1995
A;Reference number: S61010
A;Accession: S61016
A;Molecule type: DNA
A;Residues: 1-881 <POH>
A;Cross-references: EMBL:Z67751; NID:g1061234; PIDN:CAA91596.1; PID:g1061241
R;Pohl, T.M.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64899
A;Accession: S65277
A;Molecule type: DNA
A;Residues: 1-881 <POW>
A;Cross-references: EMBL:Z73604; NID:g1370510; PIDN:CAA97969.1; PID:g1370511; GSPDB:G
A;Experimental source: strain S288C (AB972)
C;Comment: This protein is a positive regulator for the gene expression of the galact
C;Genetics:
A;Gene: SGD:GAL4; MIPS:YPL248c
A;Cross-references: SGD:S0006169; MIPS:YPL248c
A;Map position: 16L
C;Superfamily: regulatory protein GAL4; GAL4 zinc binuclear cluster homology
C;Keywords: DNA binding; galactose utilization; transcription regulation; zinc finger
F;6-43/Domain: GAL4 zinc binuclear cluster homology <GAL4>
F;11-38/Region: zinc finger CCCC motif

Alignment Scores:
Pred. No.:              12.6            Length:        881
Score:                  55.00           Matches:       11
Percent Similarity:     56.67%          Conservative:  6
Best Local Similarity:  36.67%          Mismatches:    13
Query Match:            25.58%          Indels:        0
DB:                     1               Gaps:          0

US-09-198-779B-1_COPY_1_121 (1-121) x RGBYG4 (1-881)

Qy      24 CAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTGTTAT 83
           ||||||:::   |||      |||:::|||   :::|||   :::|||   |||
Db     270 GlnIleGluIleAlaSerLysAspGlnTrpGlnIleLeuPheAsnCysIleLeuAlaIle 289

Qy      84 TAATGTTGTATAATTGAGCAGGACACAACA 113
                     ||||||   ::::::|||
Db     290 GlyAlaTrpCysIleGluGlyGluSerThr 299

RESULT 8
B44110
mycocerosate synthase (EC 2.3.1.111) - Mycobacterium bovis
C;Species: Mycobacterium bovis
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 26-May-2000
C;Accession: B44110
R;Mathur, M.; Kolattukudy, P.E.
J. Biol. Chem. 267, 19388-19395, 1992
A;Title: Molecular cloning and sequencing of the gene for mycocerosic acid synthase,
-Guerin.
A;Reference number: A44110; MUID:92406887; PMID:1527058
A;Accession: B44110
A;Molecule type: DNA; protein
A;Residues: 1-2110 <MAT>
A;Cross-references: GB:M95808; NID:g149977; PIDN:AAA25369.1; PID:g149980
A;Note: sequence extracted from NCBI backbone (NCBIN:113897, NCBIP:113899)
A;Note: the source is designated as Mycobacterium tuberculosis var. bovis Bacillus Ca
C;Superfamily: mycocerosic acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I
nase homology; [acyl-carrier-protein] S-malonyltransferase homology
C;Keywords: acyltransferase; carrier protein; coenzyme A; phosphotransferase
F;27-426/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
F;534-815/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F;1443-1732/Domain: long-chain alcohol dehydrogenase homology <LADH>
F;1764-1944/Domain: short-chain alcohol dehydrogenase homology <SADH>
F;2015-2095/Domain: acyl carrier protein homology <ACP1>

Alignment Scores:
Pred. No.:              15.2            Length:        2110
Score:                  54.50           Matches:       12
```

```
Percent Similarity:     62.86%          Conservative:  10
Best Local Similarity:  34.29%          Mismatches:    8
Query Match:            25.23%          Indels:        5
DB:                     2               Gaps:          1

US-09-198-779B-1_COPY_1_121 (1-121) x B44110 (1-2110)

Qy    107 GTCCTGCTCAATTATACAACATTAATAACACAACGAACAATGGATCAGGACCGTCCATTT 48
          :::|||:::         ::::::|||   :::||||||:::|||   ||||||   |||
Db   2033 LeuLeuValGluGlnAlaSerValIleLeuArgArgThrIleAspAlaAspArgSerPhe 2052

Qy     47 ATC--------------AGCATGGGCAGCGTCGATCTGTCCACC 18
          |||              |||:::|||   :::::::::   |||
Db   2053 IleGluTyrGlyLeuAspSerLeuGlyMetLeuGluMetArgThr 2067

RESULT 9
A70668
mycocerosate synthase (EC 2.3.1.111) - Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: A70668
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: A70668
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-2111 <COL>
A;Cross-references: GB:Z83858; GB:AL123456; NID:g3261675; PIDN:CAB06108.1; PID:g3261676
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: mas
C;Superfamily: mycocerosic acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I ho
nase homology; [acyl-carrier-protein] S-malonyltransferase homology
C;Keywords: acyltransferase; carrier protein; coenzyme A; phosphotransferase
F;27-426/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
F;534-815/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F;1444-1733/Domain: long-chain alcohol dehydrogenase homology <LADH>
F;1765-1945/Domain: short-chain alcohol dehydrogenase homology <SADH>
F;2016-2096/Domain: acyl carrier protein homology <ACP1>

Alignment Scores:
Pred. No.:              15.2            Length:        2111
Score:                  54.50           Matches:       12
Percent Similarity:     62.86%          Conservative:  10
Best Local Similarity:  34.29%          Mismatches:    8
Query Match:            25.23%          Indels:        5
DB:                     2               Gaps:          1

US-09-198-779B-1_COPY_1_121 (1-121) x A70668 (1-2111)

Qy    107 GTCCTGCTCAATTATACAACATTAATAACACAACGAACAATGGATCAGGACCGTCCATTT 48
          :::|||:::         ::::::|||   :::||||||:::|||   ||||||   |||
Db   2034 LeuLeuValGluGlnAlaSerValIleLeuArgArgThrIleAspAlaAspArgSerPhe 2053

Qy     47 ATC--------------AGCATGGGCAGCGTCGATCTGTCCACC 18
          |||              |||:::|||   :::::::::   |||
Db   2054 IleGluTyrGlyLeuAspSerLeuGlyMetLeuGluMetArgThr 2068

RESULT 10
C86926
probable mycocerosic synthase [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 24-May-2001
C;Accession: C86926
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Qavies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: C86926
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2116 <STO>
A;Cross-references: GB:AL450380; NID:g13092517; PIDN:CAC29647.1; GSPDB:GN00147
C;Genetics:
A;Gene: mas
C;Superfamily: mycocerosic acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I
nase homology; [acyl-carrier-protein] S-malonyltransferase homology
C;Keywords: carrier protein

Alignment Scores:
Pred. No.:              15.2            Length:        2116
Score:                  54.50           Matches:       12
Percent Similarity:     62.86%          Conservative:  10
Best Local Similarity:  34.29%          Mismatches:    8
Query Match:            25.23%          Indels:        5
DB:                     2               Gaps:          1

US-09-198-779B-1_COPY_1_121 (1-121) x C86926 (1-2116)

Qy    107 GTCCTGCTCAATTATACAACATTAATAACACAACGAACAATGGATCAGGACCGTCCATTT 48
          :::|||:::         ::::::|||   :::||||||:::|||   ||||||   |||
Db   2032 LeuLeuValGluGlnAlaSerValIleLeuArgArgThrIleAspAlaAspArgSerPhe 2051

Qy     47 ATC--------------AGCATGGGCAGCGTCGATCTGTCCACC 18
          |||              |||:::|||   :::::::::   |||
Db   2052 IleGluTyrGlyLeuAspSerLeuGlyMetLeuGluMetArgThr 2066

RESULT 11
S22652
transcription factor Brn-2 - African clawed frog
N;Alternate names: class III POU domain protein brain-2; transcription factor POU3
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C;Accession: S22652
R;Baltzinger, M.; Payen, E.; Remy, P.
Nucleic Acids Res. 20, 1993, 1992
A;Title: Nucleotide sequence of XLPOU3 cDNA, a member of the POU domain gene family e
A;Reference number: S22652; MUID:92253425; PMID:1579504
A;Accession: S22652
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-382 <BAL>
A;Cross-references: EMBL:X64835; NID:g65020; PIDN:CAA46047.1; PID:g65021
A;Note: this sequence was submitted to the EMBL Data Library, March 1991
C;Superfamily: transcription factor Brn-1; homeobox homology; POU domain homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;103-115/Region: histidine/proline-rich
F;208-275/Domain: POU domain homology <POU>
F;294-350/Domain: homeobox homology <HOX>

Alignment Scores:
Pred. No.:              17.6            Length:        382
Score:                  54.00           Matches:       10
Percent Similarity:     56.52%          Conservative:  3
Best Local Similarity:  43.48%          Mismatches:    10
Query Match:            25.00%          Indels:        0
DB:                     1               Gaps:          0

US-09-198-779B-1_COPY_1_121 (1-121) x S22652 (1-382)

Qy     93 TACAACATTAATAACACAACGAACAATGGATCAGGACCGTCCATTTATCAGCATGGGCAG 34
          :::   :::|||         |||   |||||||||      |||:::   ||||||
Db    146 PheThrValAsnGlyMetIleAsnProGlySerGlyGlnGlyIleHisHisHisGlyLeu 165

Qy     33 CGTCGATCT 25
          |||   |||
Db    166 ArgAspSer 168
```

RESULT 12
T08708
hypothetical protein DKFZp564D116.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C;Accession: T08708
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, March 1999
A;Reference number: Z16471
A;Accession: T08708
A;Molecule type: mRNA
A;Residues: 1-616 <WAM>
A;Cross-references: EMBL:AL050022
A;Experimental source: fetal brain; clone DKFZp564D116
C;Genetics:
A;Note: DKFZp564D116.1

Alignment Scores:

Pred. No.:	17.7	Length:	616
Score:	54.00	Matches:	12
Percent Similarity:	50.00%	Conservative:	4
Best Local Similarity:	37.50%	Mismatches:	10
Query Match:	25.12%	Indels:	6
DB:	2	Gaps:	2

US-09-198-779B-1_COPY_1_121 (1-121) x T08708 (1-616)

```
Qy      21 GGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATC------CATTGTTCG 74
           |||      |||   |||           ||||||   ::::::      |||||||||
Db     472 GlyAsnAlaAspProAlaGlnLysGlyGlyTrpThrArgIleLeuAsnArgHisCysSer 491

Qy      75 TTG------------TGTTATTAATGTTGTATAATT 98
           :::            |||      ||||||:::|||
Db     492 IleSerAlaIleAsnCysThrSerCysCysLeuIle 503
```

RESULT 13
T15597
hypothetical protein C25A11.4b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15597
R;Favello, T.
submitted to the EMBL Data Library, October 1995
A;Description: The sequence of C. elegans cosmid C25A11.
A;Reference number: Z18375
A;Accession: T15597
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-737 <FAV>
A;Cross-references: EMBL:U39650; NID:g1049376; PID:g1049381; PIDN:AAA80392.1; CESP:C25A1
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:C25A11.4b
A;Introns: 65/3; 88/3; 126/3; 433/2; 494/2; 711/2

Alignment Scores:

Pred. No.:	17.7	Length:	737
Score:	54.00	Matches:	11
Percent Similarity:	50.00%	Conservative:	3
Best Local Similarity:	39.29%	Mismatches:	14
Query Match:	25.00%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_1_121 (1-121) x T15597 (1-737)

```
Qy      99 CAATTATACAACATTAATAACACAACGAACAATGGATCAGGACCGTCCATTTATCAGCAT 40
           :::|||||||||   |||:::         |||||||||      |||   ||||||
Db     697 ArgLeuTyrAsnProAsnAspLeuAsnArgAsnGlySerSerArgSerArgTyrGlnArg 716

Qy      39 GGGCAGCGTCGATCTGTCCACCGA 16
           :::           |||
Db     717 AlaLysAsnGluLysAlaArgArg 724
```

RESULT 14
T22306
hypothetical protein F46C5.6 - Caenorhabditis_elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T22306; T24911
R;Thomas, K.
submitted to the EMBL Data Library, September 1995
A;Reference number: Z19544
A;Accession: T22306
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-849 <WIL>
A;Cross-references: EMBL:Z54281; PIDN:CAA91051.1; GSPDB:GN00020; CESP:F46C5.6
A;Experimental source: clone F46C5
R;Burton, J.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19953
A;Accession: T24911
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-849 <WI2>
A;Cross-references: EMBL:Z81123; PIDN:CAB03367.1; GSPDB:GN00020; CESP:F46C5.6
A;Experimental source: clone T14D7
C;Genetics:
A;Gene: CESP:F46C5.6
A;Map position: 2
A;Introns: 32/1; 57/3; 106/2; 175/2; 196/1; 218/1; 242/3; 278/2; 314/2; 356/1; 467/1;
C;Superfamily: Caenorhabditis elegans hypothetical protein F46C5.6

Alignment Scores:

Pred. No.:	17.8	Length:	849
Score:	54.00	Matches:	13
Percent Similarity:	53.85%	Conservative:	8
Best Local Similarity:	33.33%	Mismatches:	14
Query Match:	25.00%	Indels:	4
DB:	2	Gaps:	2

US-09-198-779B-1_COPY_1_121 (1-121) x T22306 (1-849)

```
Qy     119 CGTACGTGTTGTGTCCTGCTCAATTATACAACATTAATAACA------CAACGAACAATG 66
           :::|||||||||         ||||||      :::::::||      ::::::   :::
Db     435 LysThrCysCys------PheAsnTyrProCysMetLeuThrMetPheLysLysHisVal 452

Qy      65 GATCAGGACCGTCCATTTATCAGCATGGGCAGCGTCGATCTGTCCACCGAGGCTAGA 9
           |||:::      ||||||:::  |||         |||         |||   |||
Db     453 AspArgLeuLeuProPheLeuGluMetPheCysThrAspHisAspGluGluValArg 471
```

RESULT 15
T15598
hypothetical protein C25A11.4a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15598
R;Favello, T.
submitted to the EMBL Data Library, October 1995
A;Description: The sequence of C. elegans cosmid C25A11.
A;Reference number: Z18375
A;Accession: T15598
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1017 <FAV>
A;Cross-references: EMBL:U39650; NID:g1049376; PID:g1049380; PIDN:AAA80391.1; CESP:C2
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:C25A11.4a
A;Introns: 65/3; 88/3; 126/3; 433/2; 494/2; 711/2; 735/1; 792/3; 833/3; 873/2

Alignment Scores:

Pred. No.:	17.8	Length:	1017
Score:	54.00	Matches:	11
Percent Similarity:	50.00%	Conservative:	3
Best Local Similarity:	39.29%	Mismatches:	14

```
Query Match:            25.00%      Indels:        0
DB:                     2           Gaps:          0

US-09-198-779B-1_COPY_1_121 (1-121) x T15598 (1-1017)

Qy      99 CAATTATACAACATTAATAACACAACGAACAATGGATCAGGACCGTCCATTTATCAGCAT 40
           :::|||||||||   |||:::         |||||||||      |||   ||||||
Db     697 ArgLeuTyrAsnProAsnAspLeuAsnArgAsnGlySerSerArgSerArgTyrGlnArg 716

Qy      39 GGGCAGCGTCGATCTGTCCACCGA 16
           :::           |||
Db     717 AlaLysAsnGluLysAlaArgArg 724

RESULT 16
T49868
related to suppressor protein SPT23 [imported] - Neurospora crassa
N;Alternate names: protein B24P11.240
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49868
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49868
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1174 <SCH>
A;Cross-references: EMBL:AL356833; GSPDB:GN00116; NCSP:B24P11.240
A;Experimental source: BAC clone B24P11; strain OR74A
C;Genetics:
A;Gene: NCSP:B24P11.240
A;Map position: 6
A;Introns: 407/1

Alignment Scores:
Pred. No.:              21.2        Length:        1174
Score:                  53.50       Matches:       12
Percent Similarity:     54.55%      Conservative:  0
Best Local Similarity:  54.55%      Mismatches:    5
Query Match:            24.77%      Indels:        5
DB:                     2           Gaps:          1

US-09-198-779B-1_COPY_1_121 (1-121) x T49868 (1-1174)

Qy      87 ATTAATAACACAACGAACAATGGATCAGGACCGTCC---------------ATTTATCAG 43
           |||   |||   ||||||   ||||||||||||||                |||
Db     648 IleGlnAsnPheThrAsnGluGlySerGlyProSerAlaSerGlyAlaProThrTyrAsn 667

Qy      42 CATGGG 37
           ||||||
Db     668 HisGly 669

RESULT 17
A87423
hypothetical protein CC1400 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: A87423
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87423
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-134 <STO>
A;Cross-references: GB:AE005673; NID:g13422759; PIDN:AAK23381.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC1400

Alignment Scores:
Pred. No.:              24.5        Length:        134
Score:                  53.00       Matches:       9
Percent Similarity:     42.31%      Conservative:  2
Best Local Similarity:  34.62%      Mismatches:    15
Query Match:            24.65%      Indels:        0
DB:                     2           Gaps:          0

US-09-198-779B-1_COPY_1_121 (1-121) x A87423 (1-134)

Qy       6 CCGTCTAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATC 65
           |||      |||   |||   :::      :::      |||   |||
Db      79 ProArgLeuLeuAlaGlyProLeuCysThrSerSerGlnAspSerTrpAlaPheAlaGly 98

Qy      66 CATTGTTCGTTGTGTTAT 83
           ||||||     ||||||
Db      99 HisCysProAlaCysTyr 104

RESULT 18
F90445
conserved hypothetical protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: F90445
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Ch
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: F90445
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-302 <KUR>
A;Cross-references: GB:AE006641; NID:g13816030; PIDN:AAK42821.1; GSPDB:GN00155
C;Genetics:
A;Gene: SSO2710

Alignment Scores:
Pred. No.:              24.8        Length:        302
Score:                  53.00       Matches:       10
Percent Similarity:     51.61%      Conservative:  6
Best Local Similarity:  32.26%      Mismatches:    15
Query Match:            24.54%      Indels:        0
DB:                     2           Gaps:          0

US-09-198-779B-1_COPY_1_121 (1-121) x F90445 (1-302)

Qy      95 TATACAACATTAATAACACAACGAACAATGGATCAGGACCGTCCATTTATCAGCATGGGC 36
           |||   |||:::               :::|||   |||   |||:::|||   :::
Db     227 TyrAsnThrIleLysArgAlaLeuGluIleAspProAspAsnProTyrIleLysLeuThr 246

Qy      35 AGCGTCGATCTGTCCACCGAGGCTAGACGGAAA 3
           |||::::::   ||||||         |||
Db     247 GluValGluIleLeuThrGluThrAsnGluLys 257

RESULT 19
B69081
acetyl-CoA synthetase - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: B69081
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani,
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: B69081
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-400 <MTH>
A;Cross-references: GB:AE000919; GB:AE000666; NID:g2622717; PIDN:AAB86076.1; PID:g262
A;Experimental source: strain Delta H
```

```
C;Genetics:
A;Gene: MTH1603
A;Start codon: TTG
C;Superfamily: acetate-CoA ligase homology
F;141-400/Domain: acetate-CoA ligase homology #status atypical <ACL>

Alignment Scores:
Pred. No.:                24.9          Length:         400
Score:                    53.00         Matches:        9
Percent Similarity:       66.67%        Conservative:   3
Best Local Similarity:    50.00%        Mismatches:     6
Query Match:              24.65%        Indels:         0
DB:                       2             Gaps:           0

US-09-198-779B-1_COPY_1_121 (1-121) x B69081 (1-400)

Qy      26 GATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGTG 79
           |||      |||||||||      :::|||      |||||||||||:::::
Db     256 AspAspGluCysProCysGlnGluLeuAspProGluAspProLeuPheIleLeu 273

RESULT 20
T24868
hypothetical protein T12G3.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24868
R;Sims, M.
submitted to the EMBL Data Library, January 1996
A;Reference number: Z19945
A;Accession: T24868
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-928 <WIL>
A;Cross-references: EMBL:Z68752; PIDN:CAA92981.1; GSPDB:GN00022; CESP:T12G3.2
A;Experimental source: clone T12G3
C;Genetics:
A;Gene: CESP:T12G3.2
A;Map position: 4
A;Introns: 39/3; 300/2; 533/3; 558/1; 640/1; 768/2; 893/3

Alignment Scores:
Pred. No.:                25.2          Length:         928
Score:                    53.00         Matches:        14
Percent Similarity:       61.29%        Conservative:   5
Best Local Similarity:    45.16%        Mismatches:     6
Query Match:              24.54%        Indels:         6
DB:                       2             Gaps:           2

US-09-198-779B-1_COPY_1_121 (1-121) x T24868 (1-928)

Qy     105 CCTGCTCAATTATACAACATTAATAACACAACG---------------AACAATGGATCA 61
           |||:::||||||   :::   |||   ||||||               |||||||||
Db     895 ProSerGlnLeuProSerProAsnGlnThrThrIleProHisMetTyrAsnAsnGlyIle 914

Qy      60 GGACCGTCCATTTATCAGCATGGGCAGCGTCGA 28
              |||   |||||||:::|||   |||::::::
Db     915 ---ProMetIleTyrGluHisHisGlnGlnGln 924

RESULT 21
D71612
hypothetical protein PFB0540w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: D71612
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: D71612
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1844 <GAR>
A;Cross-references: GB:AE001401; GB:AE001362; NID:g3845209; PIDN:AAC71897.1; PID:g384
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0540w

Alignment Scores:
Pred. No.:                25.4          Length:         1844
Score:                    53.00         Matches:        10
Percent Similarity:       53.85%        Conservative:   4
Best Local Similarity:    38.46%        Mismatches:     12
Query Match:              24.54%        Indels:         0
DB:                       2             Gaps:           0

US-09-198-779B-1_COPY_1_121 (1-121) x D71612 (1-1844)

Qy      90 AACATTAATAACACAACGAACAATGGATCAGGACCGTCCATTTATCAGCATGGGCAGCGT 31
           |||   ||||||      ||||||   :::      ||||||      :::
Db     881 AsnAsnAsnAsnAsnAsnAsnAsnAsnAsnHisSerIleIleAsnAsnAsnIleThr 900

Qy      30 CGATCTGTCCACCGAGGC 13
           :::   :::|||||||||
Db     901 GlnGlyIleHisArgGly 906

RESULT 22
T13049
eyelid - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13049
R;Treisman, J.E.; Luk, A.; Rubin, G.M.; Heberlein, U.
submitted to the EMBL Data Library, March 1998
A;Reference number: Z17592
A;Accession: T13049
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2715 <TRE>
A;Cross-references: EMBL:AF053091; NID:g2981220; PID:g2981221; PIDN:AAC06254.1
C;Genetics:
A;Gene: eld
A;Cross-references: FlyBase:FBgn0003013
C;Function:
A;Description: could act as a transcription factor antagonistic to the Wg pathway
C;Keywords: DNA binding

Alignment Scores:
Pred. No.:                25.6          Length:         2715
Score:                    53.00         Matches:        10
Percent Similarity:       78.57%        Conservative:   1
Best Local Similarity:    71.43%        Mismatches:     3
Query Match:              24.54%        Indels:         0
DB:                       2             Gaps:           0

US-09-198-779B-1_COPY_1_121 (1-121) x T13049 (1-2715)

Qy      84 AATAACACAACGAACAATGGATCAGGACCGTCCATTTATCAG 43
           ||||||   :::|||||||||||||   |||||||||  . |||
Db      46 AsnAsnAsnSerAsnAsnGlySerAspProSerIleGlnGln 59

RESULT 23
G95375
probable drug resistance protein [imported] - Sinorhizobium meliloti (strain 1021) ma
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: G95375
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; B
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: G95375
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-388 <KUR>
```

```
A;Cross-references: GB:AE006469; PIDN:AAK65569.1; PID:g14524048; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMa1664
A;Genome: plasmid

Alignment Scores:
Pred. No.:                35.2          Length:          388
Score:                    52.00         Matches:         12
Percent Similarity:       58.33%        Conservative:    9
Best Local Similarity:    33.33%        Mismatches:      14
Query Match:              24.07%        Indels:          1
DB:                       2             Gaps:            0

US-09-198-779B-1_COPY_1_121 (1-121) x G95375 (1-388)

Qy    114 GTGTTGTGTCCTGCTCAATTATACAACATTAATAACACAACGAACAATGGATCAGGACCG 55
          :::|||   |||   ||| :::   |||:::|||   :::            ::::::||
Db    278 LeuLeuMetProGlyGln-PheValThrValIleValGluProGluGluArgGluGluAr 297

Qy     54 TCCATTTATCAGCATGGGCAGCGTCGATCTGTCCACCGAGGCTAGA 9
          ||||   :::   :::||||||||||:::         |||   |||
Db    297 gProValValProValGlySerValGluGlnAspArgGluGlyArg 312

RESULT 24
G83916
glycolate oxidase iron-sulfur subunit BH2135 [imported] - Bacillus halodurans (strain C-
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: G83916
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83916
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-451 <STO>
A;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05854.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2135
C;Superfamily: Synechocystis (S)-2-hydroxy-acid oxidase

Alignment Scores:
Pred. No.:                35.2          Length:          451
Score:                    52.00         Matches:         11
Percent Similarity:       45.16%        Conservative:    3
Best Local Similarity:    35.48%        Mismatches:      15
Query Match:              24.19%        Indels:          2
DB:                       2             Gaps:            1

US-09-198-779B-1_COPY_1_121 (1-121) x G83916 (1-451)

Qy      6 CCGTCTAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGAT------AAATGGACGGTC 59
          |||   ||||||                 :::   |||   |||      ||||||
Db     11 ProProSerLeuThrAsnTyrHisTrpSerAspHisProAspProAsnLysTrpAlaAsp 30

Qy     60 CTGATCCATTGTTCGTTGTGTTATTAATGTTGT 92
             :::||||||   :::|||        |||
Db     31 CysValHisCysGlyMetCysLeuGluAlaCys 41

RESULT 25
S17998
gene COX1 intron 4 protein - yeast (Kluyveromyces marxianus var. lactis) mitochondrio
C;Species: mitochondrion Kluyveromyces marxianus var. lactis, Candida sphaerica
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 08-Sep-2000
C;Accession: S17998
R;Hardy, C.M.; Clark-Walker, G.D.
Curr. Genet. 20, 99-114, 1991
A;Title: Nucleotide sequence of the COX1 gene in Kluyveromyces lactis mitochondrial D
A;Reference number: S17993; MUID:92035081; PMID:1657415
A;Accession: S17998
A;Molecule type: DNA
A;Residues: 1-763 <HAR>
A;Cross-references: EMBL:X57546
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC2
A;Introns: 69/1; 235/3; 324/2
C;Superfamily: cytochrome-c oxidase chain I homology
C;Keywords: mitochondrion
F;1-369/Region: cox1 exons 1 to 4 encoded
F;370-763/Region: cox1 intron encoded

Alignment Scores:
Pred. No.:                35.5          Length:          763
Score:                    52.00         Matches:         9
Percent Similarity:       75.00%        Conservative:    3
Best Local Similarity:    56.25%        Mismatches:      4
Query Match:              24.07%        Indels:          0
DB:                       2             Gaps:            0

US-09-198-779B-1_COPY_1_121 (1-121) x S17998 (1-763)

Qy    114 GTGTTGTGTCCTGCTCAATTATACAACATTAATAACACAACGAACAAT 67
          :::|||         ::::::|||||||||||||||   |||||||||
Db    408 IleLeuTyrSerIleLysMetTyrAsnIleAsnAsnAsnThrAsnAsn 423

RESULT 26
C75585
carboxylase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: C75585
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: C75585
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1091 <WHI>
A;Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12468.1; PID:g646
A;Experimental source: strain R1
C;Genetics:
A;Gene: DRA0310
A;Map position: 2

Alignment Scores:
Pred. No.:                35.7          Length:          1091
Score:                    52.00         Matches:         11
Percent Similarity:       80.00%        Conservative:    1
Best Local Similarity:    73.33%        Mismatches:      3
Query Match:              24.19%        Indels:          0
DB:                       2             Gaps:            0

US-09-198-779B-1_COPY_1_121 (1-121) x C75585 (1-1091)

Qy      6 CCGTCTAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAA 50
          |||:::   |||||||||   ||||||||||||   |||||||||
Db    902 ProAlaValLeuGlyGlyAlaIleAspAlaAlaGlyAlaAspLys 916

RESULT 27
S48424
```

```
hypothetical protein YIL055c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 19-Apr-2002
C;Accession: S48424
R;Smith, V.
submitted to the EMBL Data Library, September 1994
A;Reference number: S48407
A;Accession: S48424
A;Molecule type: DNA
A;Residues: 1-627 <SMI>
A;Cross-references: GB:Z47047; EMBL:Z38060; NID:g603997; PID:g763291; GSPDB:GN00009; MIP
C;Genetics:
A;Gene: MIPS:YIL055c
A;Cross-references: SGD:S0001317
A;Map position: 9L

Alignment Scores:
Pred. No.:                42.1          Length:          627
Score:                    51.50         Matches:         11
Percent Similarity:       64.29%        Conservative:    7
Best Local Similarity:    39.29%        Mismatches:      7
Query Match:              23.84%        Indels:          3
DB:                       2             Gaps:            1

US-09-198-779B-1_COPY_1_121 (1-121) x S48424 (1-627)

Qy      96 TTATACAACATTAAT---------AACACAACGAACAATGGATCAGGACCGTCCATTTAT 46
           |||||||||:::|||         |||:::   ||||||||||:::   |||:::
Db     329 LeuTyrAsnLeuAsnMetAlaSerAsnSerAsnAsnAsnGlyAsnIleProThrThrSer 348

Qy      45 CAGCATGGGCAGCGTCGATCTGTC 22
              :::|||      |||::::::
Db     349 ThrAsnGlyAspAspArgAlaLeu 356

RESULT 28
T24216
chromosome condensation protein homolog DPY-27 - Caenorhabditis elegans
N;Alternate names: protein R13G10.1
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Jun-2000
C;Accession: T24216; A55095
R;Gardner, A.
submitted to the EMBL Data Library, August 1994
A;Reference number: Z19857
A;Accession: T24216
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1469 <WIL>
A;Cross-references: EMBL:Z35602; PIDN:CAA84669.1; GSPDB:GN00021; CESP:R13G10.1
A;Experimental source: clone R13G10
R;Chuang, P.T.; Albertson, D.G.; Meyer, B.J.
Cell 79, 459-474, 1994
A;Title: DPY-27:a chromosome condensation protein homolog that regulates Caenorhabditis
A;Reference number: A55095; MUID:95042743; PMID:7954812
A;Accession: A55095
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1132,'G',1134-1469 <CHU>
A;Cross-references: GB:L35274; NID:g529384; PIDN:AAA62647.1; PID:g529385
A;Note: authors translated the codon GAT for residue 1133 as Gly
C;Genetics:
A;Gene: CESP:R13G10.1
A;Map position: 3
A;Introns: 142/3; 176/3; 296/2; 548/2; 627/3; 697/2; 847/3; 993/3; 1086/2; 1202/3; 1383/
C;Superfamily: chromosome segregation protein SMC1

Alignment Scores:
Pred. No.:                42.6          Length:          1469
Score:                    51.50         Matches:         12
Percent Similarity:       57.69%        Conservative:    3
Best Local Similarity:    46.15%        Mismatches:      8
Query Match:              23.84%        Indels:          3
DB:                       2             Gaps:            1

US-09-198-779B-1_COPY_1_121 (1-121) x T24216 (1-1469)

Qy      71 ACAATGGATCAGGACCGTCCATTTATC---------AGCATGGGCAGCGTCGATCTGTCC 21
           |||   |||   |||||||||:::            ||||||      |||||||||
Db      10 ThrSerAspAspAspArgProTyrAlaAspThrAspSerMetProGluValAspLeuAsp 29

Qy      20 ACCGAGGCTAGACGGAAA 3
              :::   ||||||:::
Db      30 ValAspArgArgArgGln 35

RESULT 29
E70522
probable polyketide synthase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: E70522
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70522
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-2126 <COL>
A;Cross-references: GB:Z97188; GB:AL123456; NID:g3261805; PIDN:CAB10012.1; PID:g22248
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: pks2
C;Superfamily: mycocerosic acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I
nase homology; [acyl-carrier-protein] S-malonyltransferase homology
C;Keywords: carrier protein
F;46-445/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
F;553-833/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F;1451-1739/Domain: long-chain alcohol dehydrogenase homology <LADH>
F;1772-1952/Domain: short-chain alcohol dehydrogenase homology <SADH>
F;2044-2109/Domain: acyl carrier protein homology <ACP1>

Alignment Scores:
Pred. No.:                42.9          Length:          2126
Score:                    51.50         Matches:         12
Percent Similarity:       65.52%        Conservative:    7
Best Local Similarity:    41.38%        Mismatches:      5
Query Match:              23.84%        Indels:          5
DB:                       2             Gaps:            1

US-09-198-779B-1_COPY_1_121 (1-121) x E70522 (1-2126)

Qy      89 ACATTAATAACACAACGAACAATGGATCAGGACCGTCCA---------------TTTATC 45
           :::||||||   :::|||||||:::|||   |||||||||
Db    2055 SerLeuIleLeuArgArgThrValAspProAspArgProLeuProGluTyrGlyLeuAsp 2074

Qy      44 AGCATGGGCAGCGTCGATCTGTCCACC 18
           |||:::|||:::::::::|||   |||
Db    2075 SerLeuGlyAlaLeuGluLeuArgThr 2083

RESULT 30
T04971
hypothetical protein T16L1.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 04-Mar-2000
C;Accession: T04971
R;Bevan, M.; Obermaier, B.; Deutschenbaur, S.; Piravandi, E.; Hoheisel, J.; Mewes, H.
submitted to the Protein Sequence Database, November 1998
A;Reference number: Z15393
A;Accession: T04971
A;Molecule type: DNA
A;Residues: 1-371 <BEV>
A;Cross-references: EMBL:AL031394
A;Experimental source: cultivar Columbia; BAC clone T16L1
```

```
C;Genetics:
A;Map position: 4
A;Introns: 69/1; 83/3; 123/3; 176/2; 201/2; 224/3; 275/3; 312/1; 333/1
A;Note: T16L1.30
C;Superfamily: Arabidopsis thaliana hypothetical protein T16L1.30

Alignment Scores:
Pred. No.:              49.7          Length:         371
Score:                  51.00         Matches:        12
Percent Similarity:     60.87%        Conservative:   2
Best Local Similarity:  52.17%        Mismatches:     9
Query Match:            23.72%        Indels:         0
DB:                     2             Gaps:           0

US-09-198-779B-1_COPY_1_121 (1-121) x T04971 (1-371)

Qy      19 GTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTTGT 78
           |||||||:::   ||||||||||:::|||   |||      |||            |||
Db     153 ValAspLysAspThrLeuProValLeuPheAsnProLeuSerPheHisPhePheArgMet 172

Qy      79 GTTATTAAT 87
           |||||||||
Db     173 ValIleAsn 175

RESULT 31
T47873
phosphatidate cytidylyltransferase-like protein - Arabidopsis thaliana
N;Alternate names: protein T4C21.30
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47873
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24479
A;Accession: T47873
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-399 <CHO>
A;Cross-references: EMBL:AL162295
A;Experimental source: cultivar Columbia; BAC clone T4C21
C;Genetics:
A;Map position: 3
A;Introns: 81/3; 185/2; 249/1; 290/3; 335/2; 374/1
A;Note: T4C21.30

Alignment Scores:
Pred. No.:              49.7          Length:         399
Score:                  51.00         Matches:        16
Percent Similarity:     52.78%        Conservative:   3
Best Local Similarity:  44.44%        Mismatches:     11
Query Match:            23.72%        Indels:         6
DB:                     2             Gaps:           2

US-09-198-779B-1_COPY_1_121 (1-121) x T47873 (1-399)

Qy       3 TTTCCGTCTAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTG 62
           :::|||:::   ||||||||||||         ||||||         |||||||||
Db     254 TrpProThrIleLeuGlyGlyGln---------AlaHis---------TrpThrValGly 267

Qy      63 ATCCATTGTTCGTTGTGTTATTAATGTTGTATAATTGAGCAGGACACA 110
           :::         |||         |||   ||||||      ||||||
Db     268 LeuValAlaIleLeuIleSerPheCysGlyIleIleAlaSerAspThr 283

RESULT 32
T32605
hypothetical protein E04A4.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32605
R;Sammons, L.; Wohldmann, P.; Biewald, T.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid E04A4.
A;Reference number: Z21199
A;Accession: T32605
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-433 <SAM>
A;Cross-references: EMBL:AF038611; PIDN:AAB92038.1; GSPDB:GN00022; CESP:E04A4.3
A;Experimental source: strain Bristol N2; clone E04A4
C;Genetics:
A;Gene: CESP:E04A4.3
A;Map position: 4
A;Introns: 21/2; 113/1; 147/3; 190/1; 283/2; 345/3; 382/3; 418/2

Alignment Scores:
Pred. No.:              49.8          Length:         433
Score:                  51.00         Matches:        10
Percent Similarity:     57.89%        Conservative:   1
Best Local Similarity:  52.63%        Mismatches:     8
Query Match:            23.72%        Indels:         0
DB:                     2             Gaps:           0

US-09-198-779B-1_COPY_1_121 (1-121) x T32605 (1-433)

Qy      20 TGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTGATCCATTGTTCGTT 76
           |||      ||||||||||||||||     :::||||||         |||   |||
Db     324 TrpGlyGlyArgArgCysProCysLeuLeuValAspGlyGluAlaAlaLeuValVal 342

RESULT 33
JQ2010
transcription factor POU-1 - planarian (Dugesia japonica)
C;Species: Dugesia japonica
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 16-Jun-2000
C;Accession: JQ2010
R;Orii, H.; Agata, K.; Watanabe, K.
Biochem. Biophys. Res. Commun. 192, 1395-1402, 1993
A;Title: POU-domain genes in planarian Dugesia japonica: the structure and expression
A;Reference number: JQ2010; MUID:93282851; PMID:8099480
A;Accession: JQ2010
A;Molecule type: mRNA
A;Residues: 1-559 <ORI>
A;Cross-references: DDBJ:D12924; NID:g217311; PIDN:BAA02308.1; PID:g217312
A;Experimental source: strain GI
C;Genetics:
A;Gene: DjPOU1
C;Superfamily: planarian transcription factor POU-1; homeobox homology; POU domain ho
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;266-333/Domain: POU domain homology <POU>
F;352-408/Domain: homeobox homology <HOX>

Alignment Scores:
Pred. No.:              50            Length:         559
Score:                  51.00         Matches:        8
Percent Similarity:     58.33%        Conservative:   6
Best Local Similarity:  33.33%        Mismatches:     10
Query Match:            23.61%        Indels:         0
DB:                     1             Gaps:           0

US-09-198-779B-1_COPY_1_121 (1-121) x JQ2010 (1-559)

Qy     105 CCTGCTCAATTATACAACATTAATAACACAACGAACAATGGATCAGGACCGTCCATTTAT 46
           |||        :::      ||||||      :::||||||:::   |||::::::::
Db     534 ProArgSerPhePheMetLysAsnAsnIleTyrSerAsnGlyThrThrProThrLeuPhe 553

Qy      45 CAGCATGGGCAG 34
           |||   |||
Db     554 AspHisSerGln 557

RESULT 34
T18649
hypothetical protein B0024.14 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18649
R;McMurray, A.
```

submitted to the EMBL Data Library, April 1996
A;Reference number: Z19001
A;Accession: T18649
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-884 <WIL>
A;Cross-references: EMBL:Z71178; PIDN:CAA94886.1; GSPDB:GN00023; CESP:B0024.14
A;Experimental source: clone B0024
C;Genetics:
A;Gene: CESP:B0024.14
A;Map position: 5
A;Introns: 46/3; 84/1; 212/1; 307/2; 345/2; 394/1; 424/2; 481/1; 596/1; 702/1; 765/3; 85

Alignment Scores:

Pred. No.:	50.3	Length:	884
Score:	51.00	Matches:	12
Percent Similarity:	54.84%	Conservative:	5
Best Local Similarity:	38.71%	Mismatches:	14
Query Match:	23.72%	Indels:	0
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_1_121 (1-121) x T18649 (1-884)

```
Qy       3 TTTCCGTCTAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCCTG 62
           ||||||:::|||||||||   ::::::|||      :::          |||   |||
Db     717 PheProThrSerLeuGlyProArgValAspAspGlyAsnGlySerSerAlaThrSerLeu 736

Qy      63 ATCCATTGTTCGTTGTGTTATTAATGTTGTATA 95
           |||      ||||||         |||   :::
Db     737 IleValValSerLeuMetSerLeuCysValVal 747
```

RESULT 35
I38968
100 kDa coactivator - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 28-Jul-2000
C;Accession: I38968
R;Tong, X.; Drapkin, R.; Yalamanchili, R.; Mosialos, G.; Kieff, E.
Mol. Cell. Biol. 15, 4735-4744, 1995
A;Title: The Epstein-Barr virus nuclear protein 2 acidic domain forms a complex with a n
A;Reference number: I38968; MUID:95379816; PMID:7651391
A;Accession: I38968
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-885 <RES>
A;Cross-references: EMBL:U22055; NID:g799176; PIDN:AAA80488.1; PID:g799177
C;Superfamily: Schizosaccharomyces pombe probable transcription factor SPCC645.08c

Alignment Scores:

Pred. No.:	50.3	Length:	885
Score:	51.00	Matches:	11
Percent Similarity:	75.00%	Conservative:	4
Best Local Similarity:	55.00%	Mismatches:	1
Query Match:	23.61%	Indels:	4
DB:	2	Gaps:	1

US-09-198-779B-1_COPY_1_121 (1-121) x I38968 (1-885)

```
Qy      61 AGGACCGTCCATTTATCAGCATGGGCAGCGTCGATCTGTCCACCGAGGCTAGACGGAAAA 2
           :::|||:::|||||||||            ||||||   ||||||||||||:::|||:::
Db     341 LysThrIleHisLeuSer----------SerIleArgProProArgLeuGluGlyGlu 356
```

RESULT 36
F81539
polymorphic membrane protein G family CP0770 [imported] - Chlamydophila pneumoniae (stra
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 15-Jun-2001
C;Accession: F81539
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: F81539
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-922 <REA>
A;Cross-references: GB:AE002237; GB:AE002161; NID:g7189684; PIDN:AAF38570.1; PID:g718
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CP0770
C;Superfamily: Chlamydophila pneumoniae polymorphic outer membrane protein G

Alignment Scores:

Pred. No.:	50.3	Length:	922
Score:	51.00	Matches:	12
Percent Similarity:	58.06%	Conservative:	6
Best Local Similarity:	38.71%	Mismatches:	12
Query Match:	23.61%	Indels:	1
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_1_121 (1-121) x F81539 (1-922)

```
Qy     102 GCTCAATTATACAACATTAATAACACAACGAACAATGGATCAGGACCGTCCATTTATCAG 43
           |||::::::            ||||||      ||||||||||||   ::::::||| ||
Db     209 AlaGluIleArgPheAlaGlnAsnThrAlaLysAsnGlySerGlyGlyAlaLeuTyr-Se 228

Qy      42 CATGGGCAGCGTCGATCTGTCCACCGAGGCT 12
           |   |||   :::|||:::         |||
Db     228 rAspGlyAspIleAspIleAspGlnAsnAla 238
```

RESULT 37
B72131
polymorphic outer membrane protein g family - Chlamydophila pneumoniae (strain CWL029
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001
C;Accession: B72131
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood,
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: B72131
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-922 <ARN>
A;Cross-references: GB:AE001585; GB:AE001363; NID:g4376255; PIDN:AAD18163.1; PID:g437
A;Experimental source: strain CWL029
C;Genetics:
A;Gene: pmp_1
C;Superfamily: Chlamydophila pneumoniae polymorphic outer membrane protein G

Alignment Scores:

Pred. No.:	50.3	Length:	922
Score:	51.00	Matches:	12
Percent Similarity:	58.06%	Conservative:	6
Best Local Similarity:	38.71%	Mismatches:	12
Query Match:	23.61%	Indels:	1
DB:	2	Gaps:	0

US-09-198-779B-1_COPY_1_121 (1-121) x B72131 (1-922)

```
Qy     102 GCTCAATTATACAACATTAATAACACAACGAACAATGGATCAGGACCGTCCATTTATCAG 43
           |||::::::            ||||||      ||||||||||||   ::::::||| ||
Db     209 AlaGluIleArgPheAlaGlnAsnThrAlaLysAsnGlySerGlyGlyAlaLeuTyr-Se 228

Qy      42 CATGGGCAGCGTCGATCTGTCCACCGAGGCT 12
           |   |||   :::|||:::         |||
Db     228 rAspGlyAspIleAspIleAspGlnAsnAla 238
```

RESULT 38
E86491
polymorphic outer membrane protein G family [imported] - Chlamydophila pneumoniae (st
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001
C;Accession: E86491
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;

```
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: E86491
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-922 <STO>
A;Cross-references: GB:BA000008; NID:g8978378; PIDN:BAA98215.1; GSPDB:GN00142
A;Experimental source: strain J138
C;Genetics:
A;Gene: pmp_1
C;Superfamily: Chlamydophila pneumoniae polymorphic outer membrane protein G

Alignment Scores:
Pred. No.:              50.3          Length:         922
Score:                  51.00         Matches:        12
Percent Similarity:     58.06%        Conservative:   6
Best Local Similarity:  38.71%        Mismatches:     12
Query Match:            23.61%        Indels:         1
DB:                     2             Gaps:           0

US-09-198-779B-1_COPY_1_121 (1-121) x E86491 (1-922)

Qy    102 GCTCAATTATACAACATTAATAACACAACGAACAATGGATCAGGACCGTCCATTTATCAG 43
          |||:::::::            ||||||      ||||||||||||   :::::::||| ||
Db    209 AlaGluIleArgPheAlaGlnAsnThrAlaLysAsnGlySerGlyGlyAlaLeuTyr-Se 228

Qy     42 CATGGGCAGCGTCGATCTGTCCACCGAGGCT 12
          |   |||   :::|||:::         |||
Db    228 rAspGlyAspIleAspIleAspGlnAsnAla 238

RESULT 39
T46237
hypothetical protein T9C5.190 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T46237
R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke,
submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23026
A;Accession: T46237
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1672 <RIE>
A;Cross-references: EMBL:AL132964
A;Experimental source: cultivar Columbia; BAC clone T9C5
C;Genetics:
A;Map position: 3
A;Introns: 591/1; 631/2; 829/2; 914/3; 1151/2; 1187/3; 1247/2; 1342/2; 1411/3; 1435/3; 1
A;Note: T9C5.190

Alignment Scores:
Pred. No.:              50.8          Length:         1672
Score:                  51.00         Matches:        10
Percent Similarity:     55.00%        Conservative:   1
Best Local Similarity:  50.00%        Mismatches:     9
Query Match:            23.61%        Indels:         0
DB:                     2             Gaps:           0

US-09-198-779B-1_COPY_1_121 (1-121) x T46237 (1-1672)

Qy     67 TGGATCAGGACCGTCCATTTATCAGCATGGGCAGCGTCGATCTGTCCACCGAGGCTAGAC 8
          ||||||   |||      |||      ||||||   :::      ||||||   ||||||
Db   1135 TrpIleSerThrAspTrpLeuArgLeuTrpAlaAspThrThrLeuProProAlaLeuAsp 1154

RESULT 40
T18144
hypothetical protein A642R - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18144
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z18806
A;Accession: T18144
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-74 <GRA>
A;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96966.1
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
A;Note: A642R

Alignment Scores:
Pred. No.:              57.7          Length:         74
Score:                  50.50         Matches:        11
Percent Similarity:     48.65%        Conservative:   7
Best Local Similarity:  29.73%        Mismatches:     6
Query Match:            23.38%        Indels:         13
DB:                     2             Gaps:           1

US-09-198-779B-1_COPY_1_121 (1-121) x T18144 (1-74)

Qy     96 TTATACAACATTAATAACACAACGAACAATGGATCAGGACCGTCCATTTAT--------- 46
          :::|||   :::   ||||||||||:::   |||:::|||   |||:::|||
Db      1 MetTyrIleMetGlyAsnThrThrSerLysGlyThrGlyGlySerValTyrValProAla 20

Qy     45 ----------------------------CAGCATGGGCAGCGTCGATCT 25
                                       |||:::     ||||||:::
Db     21 IleArgSerGlyLysCysSerLysValProGlnTyrAlaAspArgArgAla 37

RESULT 41
AD1012
conserved hypothetical protein STY4409 [imported] - Salmonella enterica subsp. enteri
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 17-May-2002
C;Accession: AD1012
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
A;Reference number: AB0502; PMID:11677608
A;Accession: AD1012
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-179 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD09197.1; PID:g16505201; GSPDB:GN00176
C;Genetics:
A;Gene: STY4409
C;Superfamily: Escherichia coli hypothetical protein b0354

Alignment Scores:
Pred. No.:              58.4          Length:         179
Score:                  50.50         Matches:        14
Percent Similarity:     58.62%        Conservative:   3
Best Local Similarity:  48.28%        Mismatches:     11
Query Match:            23.49%        Indels:         1
DB:                     2             Gaps:           1

US-09-198-779B-1_COPY_1_121 (1-121) x AD1012 (1-179)

Qy      1 GTTTTCCGTCTAGCCTCGGTGGACAGATCGACGCTGCCCATGCTGATAAATGGACGGTCC 60
          |||   :::         |||||||:::   |||         ||||||||||||||
Db     98 ValIleLysLysIleAspValAspLysLeuThrGlnThrGlnLeuIleAsnGlyArgLeu 117

Qy     61 TGATCCATTGTTCGTTGTGTTATTAAT 87
              :::|||   |||   |||||||||
Db    118 ---AlaIleAlaArgLeuValIleAsn 125

RESULT 42
T49596
related to H+-transporting ATP synthase chain b precursor [imported] - Neurospora cra
N;Alternate names: protein B3E4.90
```

C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49596
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49596
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-259 <SCH>
A;Cross-references: EMBL:AL355931; GSPDB:GN00116; NCSP:B3E4.90
A;Experimental source: BAC clone B3E4; strain OR74A
C;Genetics:
A;Gene: NCSP:B3E4.90
A;Map position: 6

Alignment Scores:

Pred. No.:	58.8	Length:	259
Score:	50.50	Matches:	10
Percent Similarity:	54.84%	Conservative:	7
Best Local Similarity:	32.26%	Mismatches:	11
Query Match:	23.38%	Indels:	3
DB:	2	Gaps:	1

US-09-198-779B-1_COPY_1_121 (1-121) x T49596 (1-259)

```
Qy      96 TTATACAACATTAATAACACAACGAACAATGGATCAGGACCGTCCATTTATCAGCATGGG 37
           ::::::|||   :::   |||   ||||||   :::|||      ::::::   ||||||
Db     217 IleHisAsnGlySerGlyThrGlnAsnAsnAsnAsnGlyAsnGlyLeuPheAsnHisGly 236

Qy      36 CAG---------CGTCGATCTGTCCACCGAGGC 13
                        |||   :::|||   |||
Db     237 ProLeuSerValSerArgAspLeuHisPheGly 247
```

RESULT 43
B97980
dihydroorotate oxidase (EC 1.3.3.1) pyrD [imported] - Streptococcus pneumoniae (strain R
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C;Accession: B97980
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: B97980
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-330 <KUR>
A;Cross-references: GB:AE007317; PIDN:AAK99670.1; PID:g15458470; GSPDB:GN00174
C;Genetics:
A;Gene: pyrD
C;Superfamily: dihydroorotate oxidase
C;Keywords: oxidoreductase

Alignment Scores:

Pred. No.:	59	Length:	330
Score:	50.50	Matches:	14
Percent Similarity:	56.00%	Conservative:	0
Best Local Similarity:	56.00%	Mismatches:	10
Query Match:	23.38%	Indels:	1
DB:	2	Gaps:	1

US-09-198-779B-1_COPY_1_121 (1-121) x B97980 (1-330)

```
Qy      86 TTAATAACACAACGAACAATGGATCAGGACCGTCCATTTATCAGCATGGGCAGCGTCGAT 27
           ||||||   |||               |||   |||   |||   ||||||   ||||||
Db     251 LeuIleArgGlnValAlaGlnThrThrAspLeuProIleIleGlyMetGlyGlyValAsp 270

Qy      26 CTGTCCACCGAGGCT 12
                ||||||||||||
```

Db 271 ---SerThrGluAla 274

RESULT 44
S39535
corticotropin-releasing hormone receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999
C;Accession: S39535
R;Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Lelias, J.M.; Kaghad, M.; le Fur, G.
FEBS Lett. 335, 1-5, 1993
A;Title: Primary structure and functional expression of mouse pituitary and human bra
A;Reference number: S39534; MUID:94063063; PMID:8243652
A;Accession: S39535
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-415 <VIT>
A;Cross-references: EMBL:X72305; NID:g436120; PIDN:CAA51053.1; PID:g436121
A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. 3 in having an a
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Alignment Scores:

Pred. No.:	59.2	Length:	415
Score:	50.50	Matches:	10
Percent Similarity:	68.75%	Conservative:	1
Best Local Similarity:	62.50%	Mismatches:	4
Query Match:	23.38%	Indels:	1
DB:	2	Gaps:	1

US-09-198-779B-1_COPY_1_121 (1-121) x S39535 (1-415)

```
Qy     108 TGTCCTGCTCAATTATACAACATTAAT---AACACAACGAACAATGGA 64
           |||||||||      |||   :::      ||||||||||||||||||
Db      68 CysProAlaPhePheTyrGlyValArgTyrAsnThrThrAsnAsnGly 83
```

RESULT 45
I58144
corticotropin-releasing factor receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Nov-1999
C;Accession: I58144
R;Chang, C.P.; Pearse, R.V.; O'Connell, S.; Rosenfeld, M.G.
Neuron 11, 1187-1195, 1993
A;Title: Identification of a seven transmembrane helix receptor for corticotropin-rel
A;Reference number: I58144; MUID:94099969; PMID:8274282
A;Accession: I58144
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-415 <RES>
A;Cross-references: GB:L25438; NID:g450298; PIDN:AAA16441.1; PID:g457615
C;Superfamily: glucagon receptor

Alignment Scores:

Pred. No.:	59.2	Length:	415
Score:	50.50	Matches:	10
Percent Similarity:	68.75%	Conservative:	1
Best Local Similarity:	62.50%	Mismatches:	4
Query Match:	23.38%	Indels:	1
DB:	2	Gaps:	1

US-09-198-779B-1_COPY_1_121 (1-121) x I58144 (1-415)

```
Qy     108 TGTCCTGCTCAATTATACAACATTAAT---AACACAACGAACAATGGA 64
           |||||||||      |||   :::      ||||||||||||||||||
Db      68 CysProAlaPhePheTyrGlyValArgTyrAsnThrThrAsnAsnGly 83
```

Search completed: April 23, 2003, 12:07:59
Job time : 16.0833 secs